Page 1

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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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February 15, 2003, 21:14:47 ; Search time 704.5 Seconds
(without alignments)
8509.834 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

1 gctcgagccatggtatggac.....gcaaggtgttattatcctag 206 09-833799-13C 206 Title: Perfect score: Sequence:

2054640 segs, 14551402878 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

em\_htg\_mam:\*
em\_htg\_vrt:\*
em\_sy:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSA project).
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AC121427 Rattus no
AL121782 Human DNA
AC084227 Homoo sapi
AC010700 Drosophil
AC124907 Eguus cab
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudioctyledons, core eudiocts,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Benchemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                   AL671990 Mouse DNA
AC060790 Homo sapi
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Bevan, M., Van Der Schueren, J., Chuang, Y.J., Aert, R., Defoor, E., Mayer, K.F.X.
Unpublished
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AC094194 H
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AC591103
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AC022189 1
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join(11310. 11466,11641. 11747,11806. 11908,12087. 12203, 12282. 12382,12470. 12572,14098. 14276)
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LLSRSHICHRQVHETVGSETYEIGGONMTPSTDVWVYDKLIGKQRKAPSMMVARKNAF
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E 2 (Dases 1 to 96574)

S EU Arabidopsis sequencing, project.

Direct Submission

Direct Submission

Submitted (23-SEP-1999) MIPS, at the Max-Planck-Institut fuer

Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Schuelle@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Bancroft,I., Mewes,H.W., Mayer,K.F.X., Lemcke,K. and Schueller,C.
Unpublished
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53.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.4%
Matches 79; Conservative
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JOURNAL
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ATT18B16
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IICLSTCFYFSKTCFSVFKLLLVCLFVPPPFSDFHMPBHVAAKIVSLVSEDGYDMLKA
WIOSGPDGKAAVFSRETLSSVRLDKSPLFIHMAHESSSYHMFYTKCLAFKNPYALYLQ
SLULAFHMCELDEAIALLDGIKDVFPHAGLLYIMLHSCAGSIPWEFYSMYKRRYYKFS
SUDLFADKLMFHINEVGRRQGTYKOSWEFEDYGEC"
complement (18054. .18605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'translation="MELTGLNPEFERVFHVAPVANLGHTKDLIVQNIERQCFNTVLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(15569. .15941,15983. .16035))
/gene="AT4g19270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join(15569. .15941,15983. .16035))
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complement(join(18054. .18605,19304. .19516))
/gene="AT4g19280"
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/db_xref="GI:3080358"
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/gene="AT4g19270"
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gene="AT4g19260"
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gene="AT4g19260"
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gene="AT4g19260"
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number=2
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                                                             1748. .11805
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2470. .12572
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/LTAIRSTALLOOR WARKYGTHRLTFWERHCPPVFDRKQCLVPPDBGYK
PPIRWPKSKDECWYRNVPYDWINKQKSNQNWIRKEGERFT PPGGGTWFPHGYSAYUD
MODLIPBRANCOTIRTALDTGCGVASAMGOBLLDRGILIVSLAPRDNHEAQVOFALERGI
MODLIPBRANCOTIRTALDTGCGVASAMGOBLLDRGILIVSLAPRDNHEAQVOFALERGI
PALLGIISTQRLPFPSNSPDWAHJCSRCLIPWTERGGYYLLEVHRILARPGGRWYLSGPP
QRSNYEKLQELLSSMCFKWYAKKDDIAVWQKSPDNLCYNKLSNDPDAYPPKCDDSLEP
BSAWYTPLFRCVVVPSPRLKKTDLESTFKPRPELHTTPREISUPVGGANGNVFKHDDSK
WKTRAKHYKKLLPAIGSDKIRNYDDNAYAGGLAAALVNDPLWVMNVVSSYAANTLEV
VPDRGILGTYHDWGASBTYPRTYDLLHVDGLCDMKYVMLEMDRILRPSGYAIIRESS
YFADSIASVAKELRRWSCRKEQTESASANBKKLICQKKLWYSSNASSETN"
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29370. .29440.29554. .29764,29856. .30051,30162. .>30337))
/gene="IIBB16.90"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comptement(join(28293. .28518,28623. .28679,28762. .29321,
29370. .29440,29554. .29764,29856. .30051,30162. .30337))
/gene="T18B16.90"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity to several hypothetical proteins - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="lack of ATG codon at beginning of homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative protein"
/protein_id="CAA16701.1"
/db_xref="G1:4455159"
/db_xref="SPTREMBL:049670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (28519. .28622)
/gene="T18B16.90"
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                                                                                                                           .23958)
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/gene="T18B16.80"
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/gene="T18B16.80"
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/gene="T18B16.80"
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/gene="T18B16.80"
/number=5
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                                                                                                                                                                                      complement (23959.
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            complement (23746.
                            /gene="T18B16.80"
                                                                complement (23813.
/gene="T18B16.80"
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                                                                                                                                                                                                                                                                                                                        gene="T18B16.80"
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23746. .23812,23906. .23958,24103. .24205,24352. .24490,
24580. .24669,24752. .24820,24906. .>24992))
/gene="IlBb16.80"
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CINLREVKSLRRMWIENIVKLIKEVIRENDILYFVFEYMECNLYQLMKDRQKLFAEADI
KWRCQVFGGLSYMHQRGYFRDLKPENLLVSKDIIKIADFGLAREVNSSPFTEYVS
TRWYRAPEVLLGSYVTSKVDWMAMAIMAELLSLRPIFPGASEABEIKICSVIGTP
TEETWLEGLNLANTINYQFPQLPGVPLSSLMPSASEDAINLIERLCSWDPSSRPTAAE
                                                                                                                                                                                                                                                                                                         complement (join(23185. .23271,23370. .23435,23538. .23646,
23746. .23812,23906. .23958,24103. .24205,24352. .24490,
24580. .24669,24752. .24820,24906. .24992))
                                                                                                                                                                        Contains ATP/GTP-binding site motif A (P-loop), pos.38-46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="lack of ATG codon at beginning of homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity to protein kinase rck, Mus musculus,
                                                                      /gene=""18B16.70"
join(21078. 21134,21397. 21984)
/gene="T18B16.70"
/note="similar to hypothetical protein sll0933,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains EST gb:N37947, N37384"
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/protein id="CAA16700.1"
/db_xxef="G21:4455158"
/db_xref="GPTREMB1:049669"
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/db_xref="GI:2828285"
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/gene="T18B16.80"
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/gene="T18B16.80"
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                                                                                                                                                                                                    contains EST gb:T14093"
                    /db_xref="taxon:3702"
/chromosome="4"
variety="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (23436.
/gene="T18B16.80"
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/gene="T18B16.80"
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/gene="T18B16.70"
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/gene="T18B16.70"
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/gene="T18B16.70"
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/gene="T18B16.80"
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complement (join(15863. .15964,16057. .16158,16421. .16561,
16655. .16699,16849. .16992,17042. .17190,17281. .17359,
17400. .17629. .17949. .1794,18166. .18230,18524. .18619,
18908. .19008,19112. .19152,19462. .19500,19714. .19829,
                                       Cambridge
                                                                                        Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 annotation be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV49 at the 5' end and overlap with ATCHRIV51 at the 3' end.
     Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                      lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridg
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
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6969. .7193,7306. .7473)}
/gene="AT4g19030"
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/gene="AT4g19040"
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Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Unpublished
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Lemcke, K. and Mayer, K.F.X.
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complement (join (15863. 15964,16057. 16158,16421. 16561, 16655., 16699,16849. 16992,17042. 17190,17281. 17359, 17400. 17626,17749. 19704. 17626,17749. 19704. 18709. 179019112. 19152,19462. 19500,19714. 18629, 20273. 20376,20501. 20566,20669. 20722,20898. 20972,
                                                                                                                                                                                                                                                                                        /translation="MSKVVYBGWMVRYGRRKIGRSYIHMRYFVLEPRLLAYYKKKPQD
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EKIESVIDQHQESQVPNGQQYVSFEKSGMDTGRTASSSDHESHLICIYLCKTRSAIS
FRFSAAEDEBDGRRSLMRRTIGGAALEDAAISEMQFSLRIFBELLEVDYLPRSCSRA
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MIVWPRDLCYVRYWRRNDDGSYGGGYNISPLKPRNGRPRTQVQHLIQIDLKGWGAGYL
PAFQQHCLLQMLNSVAGLREWFSQTDERGVHTRIPVMVNMASSSLSLTKSGKSLHKSA
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RPEEBPAHTD DLSCFGGNLKRRNBENBRNCWR, SDGNNFKVRGNRFGREKRPYRPCF
CPFNT IRKT PAGKHLMDLVAVLRWFKDSKR IDHVARRKGCAAQVAAEKGLFSMVNVVQV
PGSTHYSMVFYFVMKELVPGSLLQRFVQGDBFRNSRLKLIFLDFVVRIDVOLGSSTVAN
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.20376,20501. .20566,20669. .20722,20898. .20972,
                                                                                                                                                                                                           codon_start=1
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/gene="AT4g19040"
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/gene="AT4g19040"
/number=2
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/gene="AT4g19040"
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/gene="AT4g19040"
/number=6
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/gene="AT4g19040"
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                                       /gene="AT4g19040"
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/gene="AT4g19040"
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/number=4
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/gene="AT4g19040"
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PFMAL4P3 321003 bp DNA linear HTG 19-AUG-1999 Plasmodium falciparum 3D7 chromosome 4, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
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Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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On Aug 24, 1999 this sequence version replaced gi:5731899.

On Aug 24, 1999 this sequence or the Malaria Project,
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P falciparum. IMPORTANT: This
sequence is unfinished and does not necessarily represent the
correct sequence. Mork on the sequence is progress and the
release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 112137 GACTCATTATATGATCACATATAAGAACAAAGGTGTGAGCCGCATCACATAGCCTATGGT 112196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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1 (bases 1 to 321003)
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.6; DB 8; Length 199382; Pred. No. 0.48;
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/gene="AT4g19040"
/number=12
complement (17749. .17904)
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/gene="AT4g19040"
/number=12
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HTG; HTGS PHASE1.
Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7.
                                                                                                                                   complement (18166.
/gene="AT4g19040"
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                     gene="AT4g19040"
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Consensus quality: 212718 bases at least Q30
Consensus quality: 214144 bases at least Q30
Estimated insert size: 215690; sum-of-contigs estimation
Quality coverage: 10.03 in Q20 bases; agarose-fp estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 15 contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC073754 216340 bp DNA linear HTG 02-SEP-2000
Mus musculus clone RP23-333L10, WORKING DRAFT SEQUENCE, 15 ordered
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 2, 2000 this sequence version replaced gi:8810371.
Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                             Db 305898 TIGTICATAAATATACACGAGGAAATTGATTATCTCATGGAAAAGGAAAATAAACATAAG 305957
                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 CAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGT 149
                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                        30 TTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAG 89
soon as it is available and the accession number will preserved.
                                                                                                                                                                                                                                                  Score 35.8; DB 2; Length 321003; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                            0; Mismatches 57; Indels
                                                                                                                                                                                      8060 others

    .321003
/organism="Plasmodium falciparum 3D7"
/strain="3D7"

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                                                                                                                                          db_xref="taxon:36329"/chromosome="4"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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                                                           Location/Qualifiers
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Sequencing of Mouse
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55.1%;
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Best Local Similarity 55.1.
Best Annual Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 238142)
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               the accession number will be represerved.

**Dy the finished sequence as soon as it is available and the accession number will be preserved.

**30204: gap of 30204 bp in length 30205 30304: gap of unknown length 10305 39160: contig of 8856 bp in length 45624 45723: gap of unknown length 45624 45723: gap of unknown length 45524 55648: gap of unknown length 55549 60391: contig of 63825 bp in length 60392 60491: contig of 4743 bp in length 60392 60491: contig of 4743 bp in length 60392 60491: contig of 4743 bp in length 60302 60491: contig of 4743 bp in length 63508 63607: gap of unknown length 63508 63607: gap of unknown length 6492 63507: contig of 433 bp in length 6492 63507: contig of 433 bp in length 6492 74574: contig of 6303 bp in length 64951: contig of 10277 bp in length 64951: contig of 10277 bp in length 64052 88214: contig of 10277 bp in length 64052 88214: contig of 10277 bp in length 64052 88214: contig of 10277 bp in length 64054 125342: contig of 61610 bp in length 610341 125443 133102: contig of 61610 bp in length 612543 133202: gap of unknown length 612543 133202: gap of unknown length 612543 133202: gap of unknown length 6133303 133202: gap of unknown length 6133303 133202: gap of unknown length 6133303 133202: gap of unknown length 615543 133302: contig of 61600 bp in length 615543 133302: gap of unknown length 615543 133302: contig of 61600 bp in length 615543 133302: gap of unknown length 6155443 133302: g
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HTG; HTGS PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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/clone lib="RPC1 mouse BAC library 23"
61558 a 48199 c 48109 g 57071 t 1403 others
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196127: gap of unknown length
216340: contig of 20213 bp in length.
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54.7%; Pred. No. 2.8;
tive 0; Mismatches 58;
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This sequence will be replaced
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clone: S594, complete sequence.
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Submitted (14-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
                         Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 11, 2002 this sequence version replaced gi:21727332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. The true order of the pieces * is not known and their order in this sequence record is
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/note="assembly_fragment:02640"
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1 52111 c 52885 g 68246 t
                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                 Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                       --- Summary Statistics
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/db_xref="taxon:10090"
/chromosome="4"
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/clone_lib="RPCI-23"
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PRI 20-NOV-1999

AP000257 32609 bp DNA linear PRI 20-NOV-19: Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,

AP000257

LOCUS . DEFINITION

AP000257/c

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Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
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Homo sapiens 2,051,516bp genomic DNA of 21q22.1 GART and AML region
Published Only in Database (1999)
(bases 1 to 100000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequencing project is supported by Japan Science Technology Corporation (3GT) and The Institute of Physical and Chemical Research (RIKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 CAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 TGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTC 164
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Homo sapiens 32,609p genomic DNA of 21q22.1
Published Only in DataBase (1999)
2 (bases 1 to 32609)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is a part of the data (ACCESSION No. AP000174
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  Direct Submission
Submitted (15-APR-1999) Mika Hirakawa, Japan Science and Technology
Corporation (JST), Advanced Databases Department; 5-3, Yonbancho,
Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                                                                                                                                                                                                                                                                                                                 Japan Science and Technology Corporation (JST)
3.3 Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/) or send
email to webmaster@www.alis.tokyo.jst.go.jp.
Location/Qualifiers
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/standard_name="D21S63"
/note="KM1712/KM2830;The location is between each flanking
site of PCR primers."
/db_xref="GDB:287574"
a 22247 c 23866 g 28977 t
                                                                                                                                                                                                           sakaki@hgc.ims.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
sequence is submitted by Human Genome Sequencing in ALIS project of
JST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100000)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
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/note="D55705;The location is between each flanking site
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Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
clone Q78C10-f32E9, segment 1/21, complete sequence.
                                                                                                                                   This sequence is conducted by Kitasato University JST sequencing Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5445,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SHGC-51915,The location is between each flanking site of PCR primers." /db_xref="GDB:6464637"
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/organism="Homo sapiens"
/db_xref="texon:9606"
/chromosome="21"
/map="21q22.1"
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14257. .14410
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Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. coli transposon insertion: The present data does not contain E. coli transposon sequences which integrated in the coli transposon sequences. We determined the boundary between the insertion and genomic sequences experimentally, removed the insertion agequences, reconstituted the present data. The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).
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AP001712 AL163257 BA000005
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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Fujjyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Homo sapiens 2,083,744bp genomic DNA of 21q22.1 (REGION:
D218226-AML CLONE RANGE: 078C10-f32E9)
Published Only in DataBase (1999)
2 (bases 1 to 100000)
2 Lattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Direct Submission
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The DNA sequence of human chromosome 21
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/db_xref="taxon:9606"
/chromosome="21"
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TITLE

AUTHORS

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.5141,5746. .5888,
. .10327,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<81, .191,539, .720,4965, ...)
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35620. .35678))
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                                             E 2 (bases 1 to 340000)

B Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Barki,M., Tayoda,A., Ishli,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Patterson,D., Reichwald,K., Rump,A., Schilhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Rawaki,K.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
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Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Submitted (10-APR-2000) Molecular Sciences Centerer, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717325.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keio University School of Medicine, Molecular Biology, * Tokyo
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Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Max-Planck Institute for Molecular Genetics,
Innestrasse 73, D-14195 Berlin, Germany,
e.mail: info-chrzl@molgen.mpg.de
UNL: http://chrzl.rz-berlin.mpg.de/
L163257: Submitted (10-Apr-2000)
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* e.mail: nshimizu@dmb-med.keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sagamihara 228-8555, Japan,
* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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Nature 405 (6784), 311-319 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                           Yaspo, M.L.
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Direct Submission

Submitted (18-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Besearch, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguelavkiy, L., Chazaro, B., Choopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Gordte, M., Graham, L., Grand-Pierre, M., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Lackoque, K., Lamazares R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maccarby, M., McEwan, P., McKernan, K., Malthews, C., Macdonald, P., Major, J., Maythews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Donnell, D., O'Liver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Seaman, S., Severti, M., Roy, A., Santcos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Tavers, M., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Volal, K., Vo, A., Vo, A., Vo, A., Vo, A., Santos, K., Wyman, D., Ye, Wull, V., Volal, V., Vo, A., Vo, A
                 Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbul,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Strays, N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Mar 14, 2002 this sequence version replaced gi:18584052. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
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------ Project_Information
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62. .67
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1234. .1302
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1303. .1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="6"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, N., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus chromosome 6, clone RP23-44607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 221585 CAAGAAAACAACTTTCTGTCAAAGATCACTAAAACCGAGACTCATCAACAGTTCCAAGT 221526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 221525 TGCAAGCCTTTCAAAATTTTACAAAGGAATCAGTTTTCCAAAGATTTCCCCCCATATTTC 221466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC087336 181773 bp DNA linear ROD 14-MAR-2
Mus musculus chromosome 6, clone RP23-44607, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 IGGGIGGAITGGCAACAACTICCTGTGACTAACAGGICCATAGTITITCACGACACTIC 164
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                                                                                                                       /rpt_family="Simple_repeat"
/rpt_type=TaNDEM
4173. .4243
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complement(4261..4374)
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complement(4965. 5141)
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/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
4142. .4168
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/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
4378. 4471
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/rpt_type=DISPERSED
4706_ .4736
/note="(T)n"
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                                                                                 142. .4168
note="(CA)n"
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/note="(TA)n"
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'note="L1ME"
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Best Local Similarity 54.88
Matches 69, Conservative
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AC087336
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JOURNAL
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AUTHORS
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SOURCE
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/rpt_family="L1VL2"
19448. .19455
100te="single clone coverage"
21386. .21550
/rpt_family="(TTTC)n"
21577. .21844
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17435. 17616
/rpt family="(TTCC)n"
7617. 17719
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1396. 1400
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[6294..16519
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complement (12197. .13113)
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                                                                                        complement (2908. .3297)
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complement (9223. .9513)
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/rpt_family="MTD"
18030. .18139
/rpt_family="GA_rich"
complement(18161. .1834
                                                                                                                                                 /rpt_family="AT_rich"
complement(6501, .6893)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                     .9222)
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(308__,9053
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9060. .21383
rpt_family="L1VL2"
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1200. .8232
                                                         rpt_family="(TAGA)n"
544. .2679
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16519. .17421
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813. .7838
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7911. .18020
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complement(17303.
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complement(9108.
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IS8420 bp DNA linear HTG 19-JUL-2002
Rattus norvegicus clone CH230-188010, *** SEQUENCING IN PROGRESS
***, 72 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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23856. 24001
/rpt_family="GA-rich"
complement(24244. 24357)
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25864. 25888
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32664. 32738
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32112. .32184
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HTG; HTGS_PHASE1.
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Best Local Similarity 52.4%
MARCHES 76; CONSERVATIVE
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P. Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, W., Garner, T., Garza, N., Harnandez, T., Harris, K., Hart, M., Harlak, P., Hames, A., Harnandez, J., Homandez, O., Hodgson, A., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Hume, J., Jodkson, L.E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martingale, A., Martinez, E., Mawhiney, E., McLeod, M.P., Marting, W., Morgan, M., Morgan, M., Mayus, D., Mitchell, T., Mohabbat, K., Morgan, M., Morgan, M., Moser, M., Noicerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Orgunye, N., Ovidoo, R., Payton, B., Payton, B., Payton, B., Payton, B., Payton, B., Payton, B., Payton, R., Payton, B., Sason, L., Sodergren, E., Soraike, T., Shoshkari, N., Noiges, N., Tamerisa, A., Tamerisa, A., Tamerisa, R., Tamerisa, R., Tamsey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wull, Y., Wul
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NOTE: This is a "working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plaamid;
Sequencing vector: plaamid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 84455 bases at least Q40
Consensus quality: 8455 bases at least Q30
Consensus quality: 91376 bases at least Q30
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contig of 1401 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-188010
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Worley, K.C.
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Marquis-Homeyer, C., Kozlowicz, A., Hawkins, M., Dixon, R. and Boyer, E.
The sequence of Homo sapiens BAC clone RP11-629A22
Unpublished (2001)
3 (bases 1 to 153551)
Waterston, R.H.
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1 (bases 1 to 1535s)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 144673 ACATAAATATTGAGAGCTAAAACCTGGGTAAATGTTCCATTTTAGACTTTGTACTTTGTA 144732
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCP. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 18, 2001 this sequence version replaced gi:14916259.
                            Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                     Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, Y., Zhao, B., Penggen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the right is RP11-127K18, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-629A22, actual end is at base position 30773 of RP11-127K18.
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Web site: https://genome.wustl.edu/gsc
Octact: sapiens@watson.wustl.edu
Contact: Summary Statistics
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'004. .7143
'note="match to EST BG911822 (NID:g14292298)"
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'note="similar to Sus scrofa EST BF191863 (NID:g11075232)"
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7004. .7320
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2097. .22241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="ERV1"
7842. .18048
249. .3235
/rpt_family="L1"
3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
23860..25086
/rpt_family="L1"
25113..25687
/rpt_family="L1"
25725..25802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="MIR"
4059. .14267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="MIR"
716. .10135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
0180. .102co
                                                                                                                                                                                                               /rpt_family="L1"
7000. 7366
                                                                                       'rpt_family="L1"
1347. .3385
                                                                                                                                                     5712. 6726
'rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L2"
3297. .13545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4059. .14267
rpt_family="L2"
6466. .17218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="L2"
3575. .13727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="L2"
3840. .13898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .18048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9649
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1948.
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AL354926 163140 bp DNA linear PRI 22-AUG-2002
Human DNA sequence from clone RPI-216J23 on chromosome 6, complete
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Lawlor, S.

Lawlor, S.

Direct Submission

Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 23, 2002 this sequence version replaced gi:11875884.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98720 AGACAATGCACTTTATTTGGTGTAATTTTGCCTGGAAATGTACAAAGAAGAGGAGTAATTCGAT 98779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 AAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GAGTICTIGGICAATITICCAGGACACAGATGATICGGICCAAGAACAGGATAATAGAACT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 153551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
28373. .28755
/rpt_family="Malk"
28835. .28946
/rote="match to EST BG717868 (NID:g13997055)"
/rpt_family="L2"
/rpt_family="L2"
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.4%; Score 33.8; Di
Best Local Similarity 52.5%; Pred. No. 7.8;
Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family="MER1_type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35194. .35252
/rpt_family="AT_rich"
35270. .35346
/rpt_family="Mariner"
                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AT_rich"
11007. .31314
                                                                                                                                                                                                                                                                          /rpt_family="Alu"
30406. .30429
/rpt_family="(A)n"
30634. .30670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="(CA)n"
9. .32557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="(A)n"
                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="Alu"
1819. .32507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="L1"
2509. .32528
                                                                                                                                                                                                    3. .30199
family="L2"
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AL354926.17 GI:22474401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AGTITITCACGACACTICCAA 167
                                                                                                                                                                                                                              rpt_family="I
0286. .30570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .33259
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL, W., SMISSPROT, Tr., TREMBL, Wp., WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group, Further information, can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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Rattus norvegicus clone CH230-363J1, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data if.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr6
RP1-216J23 is from the library RPCI-1 constructed by the group of pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buak, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, F., Carter, M., Cavazos, S.R., Chacke, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.4%; Score 33.8; DB 9; Length 163140; 58.4%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 85293 AGAAAGAAAGAAAAGTGAGTAGTAGTGACATCAAACTACC 85253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP1-216J23"
/clone_lib="RPCI-1"
51164 a 30202 c 31236 g 50538 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ***, 46 unordered pieces. AC117956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC117956.4 GI:21746225
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Deland, A.L., Dinh, H.H., Delande, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durtin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Perfagi, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, R., Hamilton, K., Harris, C., Hartis, K., Have, M., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jouke, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Lidharge, O., Lieu, C., Liu, W., Loulseged, H., Lozado, R.J., Lucier, R., Martindale, A., Martinez, E., Mansey, B., Mawhiney, E., McLeod, M.P., Meador, M., Maju, Moser, M., Nal, D., Newtson, V., Nowtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Pace, A., Edyton, B., Perey, J., Peres, L., Peters, L., Pickerson, E., Pace, A., Payton, B., Perey, J., Peters, C., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Stone, H., Stone, H., Sudezgen, E., Sutten, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tang, H., Sutten, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Taylor, C., Walliamson, A., Wardez, W., Walliamson, A., Wardez, K., Wardhington, C., Walliamson, A., Wardez, S., Warren, R., Washington, C., Walliamson, A., Warder, S., Warren, R., Washington, C., Walliamson, A., Wardez, S., Marren, R., Washington, C., Walliamson, A., Wardez, S., Marren, R., Washington, C., Walliamson, A., Wardez, S., Marren, R., Washington, C., Walliamson, A., Warder, S., Warren, R., Warden, S., Warlen, S., Warren, R., Warden, S., Warten, S., Warten, R., Walliamson, A., Warder, S., Warren, R., Walliams, S., Warten, R., Walliams, S., Warden, S., Warten, R., Walliams, S., Warden, S., W
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Submitted (12-APR-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 169242)
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On Jul 14, 2002 this sequence version replaced gi:20260719.
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Sequencing vector: Plasmid;
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Consensus quality: 139519 bases at least Q20
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Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-363J1
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Direct Submission
Submitted (22-OCT-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (December 1 to 34122)
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Submitted (05-OCT-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 124344 AGTICITIGGGCAAGTITICTTGCAATCGCTGTTTTACTACAAGTTGAGCTCAACAATGCTA 124403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 AGTICITGGICAATTTCCAGGACACAGATGATTCGGICCAAGAACAGGATAATAGAACTA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%; Score 33.6; DB 2; Length 169242; 59.4%; Pred. No. 9.1;
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Caenorhabditis elegans cosmid Y66H1B, complete sequence.
AF100673
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 34122)
89213: contig of 6640 bp in length
89213: gap of unknown length
96070: contig of 6730 bp in length
96170: gap of unknown length
103115: contig of 7045 bp in length
103115: contig of 7045 bp in length
103115: contig of 5679 bp in length
108994: contig of 5679 bp in length
108994: contig of 8679 bp in length
10996: gap of unknown length
10996: gap of unknown length
109994: gap of unknown length
10998: contig of 8569 bp in length
10998: contig of 8680 bp in length
10998: gap of unknown length
10998: gap of unknown length
10988: lassoric contig of 8680 bp in length
1098: lassoric contig of 10348 bp in length
10998: lassoric contig of 10348 bp in length
10998: lassoric contig of 10348 bp in length
100041: length
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db xref="taxon:10116"
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| 29816 c 28876 g 47557 t
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Caenorhabditis elegans
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Waterston, R.
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Submitted (29-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
Submitted by:
  5 (bases 1 to 34122)
                     Waterston, R.
Direct Submission
                                             TITLE
JOURNAL
                   AUTHORS
REFERENCE
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COMMENT

Genome Sequencing Center

Department of Genetics, Washington University St. Louis, MO 63110, USA, and Canger Centre, Hinxton Hall Cambridge CB10 IRQ, England

email: rw@nematode.wustl.edu and jes@sanger.ac.uk

This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections e. or longer because we provide a small overlap between neighboring submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

http://www.wormbase.org/db/seq/sequence?name=Y66H1B;class=Sequence For a graphical representation of this cosmid sequence and its analysis see:

## NEIGHBORING COSMID INFORMATION

The 5' cosmid is F18F11, 200 bp overlap; the 3' cosmid is T07A9, 200 bp overlap. Actual end of this cosmid is at base position 8178 of W03G1.

## NOTES:

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.dbi.nig.ac.jp/c-elegans/html/CE INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other protains from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions, are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

source FEATURES

gene

CDS

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join[1319. 1790,2479. .2603,2649. .2870,3633. .4037,
4850. .5214,5300. .5494,5544. .5714,5758. .6358,6690. .6782,
6844. .6916,7173. .7382,7433. .7687,8240. .8383,8429. .8517,
8619. .8859,9438. .9586,9665. .9770)
                                                                                                                                                                                                                        /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=Y66H1B.1;clas
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains similarity to cadherins (Pfam:
cadherin.hmm, scores: 49.09, 38.40, 12.65, 13.42, 18.01,
60.83, 11.73, 12.81, 23.83 and 25.46)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical protein Y66H1B.1"
1. .34122
/organism="Caenorhabditis elegans"
                                                                                 db_xref="taxon:6239"
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                                                                                                                                                                     1319. .9770
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STSTHALODINDNSPYENSYSTEDLDANISPGGITGRLEATDBOSTSPNNYVTTSG
DFRETVSDSGEILFTGEGTLEKSASLEFNVTAODGGOPMNSANALLVINEHSKMKSIE
NELTTOINSNDTGGEKSEIKMLNAGMPGYTYEIIRASADGFSDSEVATWISIDSKKGR
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ATTATATOINSNDTGGEKSEIKMLNAGMPGYTYEIIRASADGFSDSEVATWISIDSKKGR
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ATTATATOINSTERGONEIKVSIKTISOPRGKLOIDRYOTEIKTSTERGIIK
GIVEGMVVKNGKAAKSSFILTILDANDNRPIFKNSSNFAVSLLESSVUGTVLIDEPYPI
EPHHEVFSYTLKYSMTGBGOFFKIDDSNSTIFKLSTERGANGGR
EPHHEVFSYTLKYSMTGBGOFFKIDDSNSTIFKLSTERDAOUGGR
EPHHEVFASVTTVINTDLTHLSTERDAOUGGVVTVLVISISDSGGVO
KTEIDVNSTLERADSDKKLVVIASLKGHAGORICSTVTATDVGGR /translation="WepKiHpslstgyfvsldnlppknlchpkslssrnegrwfiisn nhvlqvksqsgqcrivlrsaaaqmtpkaspiaqklxiipkfekseyqfqvvenreptvl gevkvisbgpvtyeilgengekfqisndgeiqnlepidretyekfelivkatdlngss ENLSNATGLOTIVDKCRONARFTLMLVHFMDINGOFTNVDRAVNLLMSSSAESRRELR SVYGLREAFPPVPIPSKVPQYILIAVLLFFVISILSMCIWCRORNNYERKLRHISAQA STVHTVTLGRGGKOTCNPGYGEIPIISRHHHPPPAPPPPTSADLQSTEL" GKSQLIIHVKDENDNSPIFDKEHYFITVDEGKSEKLKITATDADSGKNGQIVYSIDQK KNTHHNPLVITPKONSIHYFDENIVYDELLKVKVLEEDGDIGNYTFRLDEMFKKDWQM FTIGEINGSLHARQAFDFEKKTVHEIKILACRINNCTSTHLFISVNDRNDNCPMFPKQ DVRLTVLENEKGKRQVGRIPAALDSDFHSDNTKVCYTTDTPLFFFSDPTLPILFTNSS FDREHKKQHQISITAYDCHLSCRDPHKPINGTIVALIDVLDINDNFPKRSEKIYYSTY VQGHVTTGSHILTVQATDLDEEPEGLKYSIRGFVRSPSHSFVAAESPISIDKSTGELS ATEILKDSSYSFTVVVTDGAGHEDTASVVISVVTYAQQTELVFDAPFELIMKNEKKIA complement (10472. .20151)

/gene="Y66H1B.2"

gene

CDS

/note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=Y66H1B.2;clas .11853, complement(join(10472, .10507,10882, .11109,11693, .1185, 11899, .12152,12214, .12746,12795, .13646,13725, .14119, 14659, .14761,15097, .15195,18017, .18597,18649, .18834, 19130, .19288,19487, .19658,19708, .20151)) s=Sequence"

/note="contains similarity to the 24 x 96 aa approximate repeats found in human filamin (BB:L44140); coded for by the following C. elegans cDNAs: yk420e9 3, yk9c12.3, yk18f8.3, yk28f1.3, yk38c7.3, yk39b2.3, yk44b9.3, yk18f8.3, yk28f1.5, yk38c7.5, yk9c12.5, yk18f8.5, yk28f1.5, yk38c7.5, yk39b2.5, yk44b9.5, yk18f8.5, yk420e9.5, yk524c6.5"

/codon start=1

/product="Hypothetical protein Y66H1B.2" /protein\_id="AAC68999.1" /db\_xref="GI:3801003"

SHLRPTINIGKLEPKSKGLÖLLDEVNGRRYNVPMKINPDGTYSTDTPLMEVGEHKLOL LEDELVWERAVERVIKGTDVNKCKAYOPGLEQAVVOBRALPELDLOGGEGGALGSMEM GPAKAESRIODRGMSKSVBYVARAPEDDYSMALNFOKDEQKEHVKGSPFRAVVDYKUP PSQITISGLDQPNYRLNQPINFVIDTSKTKDLPVKATVPSDFAQLQPVVSRSPSNPRH HNVREVPSGKPNVSIPIĒIIYDGLKIDEKLVKVLPEVBPQLIKĪLHDKKKOSLTTTPI TYRABHGRHVPPDVRDCGRVKKIESRYPGPDGAREKLHNYSTPEDGRIYDVSFPTDRAG EYCVVFYINOGDVJARVPVMARKIGRKEDVIKEBIVPHPĒJABHSPTPVLTVHPIDAK KKKAHPAIQVLAAKPDAVRLEHIQELVDNGHRVADRIVFTATKLGTNTLDVFYGGEHV DHVEYEAIGKLEYERIQAERAKVVVEKEDDVDKYEKQYKFNVRDLGYQPKDLEAIVMP PTQKKEVAEIIDNLDGTILVKYTPKVHGSHELSILQNGAQLQGTPIKFYVDAYGDGWA TVYGPGLQNAVVGEPATFTVCAKGSQAKELSVSIEGPAKSQIKIHDNKDGTCSAAWVP PVPGEYKVHVKLGGKAVKDSPFRVLVMGEGQKRSHLSVGSTSEVALPITQQELKGISA SIKSPGGIEEPCFVRLLDGGRLGVSFTPREAGEHLITVKRDGKLVPKAPFKIKVDKTQ VGDASKVEVSGSGKAKGITLQANELLVDTSKAGYGGLSVSVQGPSKAELTCKEVKSGL IKVLYTPTEPGVYAIAIKFADHHVKDSPLTVQCTGKSAGRVIQTIQKDVEQHGICLPD QESHLFLKLLNTSPMDITARLMDPKGHTDDIEMRDLGQQYYQLKFTPKMEGIHTLSVM YKDAHVNGSPFQFTVGSFSEGGAHKVRAAGQGVVRGETGTFNAFNIYHREAGVGAVAV TIEGPSKATLEFKDHNDGNCHVDYKVATPGEVVVAVKFNDQHIPDSPFKVYIAPATGE VRKLELAQPHGQGIPAGKAFTFTVLTHRAKGHLEAKVVTPNNEVDTIDIVPIEDGESY AMRFVPKETGNHFIHVTLDGAPMRESPFRLRVGGKDLCDPTAISASGDGLVKGTTGQK /translation="MSLKKQSLKFRYYTLKCWFLKATLKSVFQFSKIKKKISENLLIG CEFVINTANAGAGILTVQMDGPSKATLDAYELEKGYKVRYTPLAPGSYPASVKYNGIH APGSPFKIPVBGKELGGNGYNETSHVKIDAVAKTSKGTVAVVPEYQGDAAKVTAKGAG LNKFFPGRPAAFQIDTGLAGTNLLANGGVYTTKGPCEEVVVRHQGSGHYVCSYRIPDRV complement (21251. .26900) KGFVFIKYGDKE1PGSPFAIEP"

gene

/gene="Y66H1B.3"

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/note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=Y66H1B.3;clas
                                                                                                                                                                                                                                                                                                                                                                                                                     KIINIDSTHIVDHNKKLILGLVWTLILHYSISMGWIQEKREDGDNKEETPKQKLLNWI
RNRLPGMPISNFTSDWNDGVALGALVNSMAPGALEDWENWSPNDALENTEKAMKSAQD
                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MAQPKRLDQEEEVVPAIRHDDAEWKIIQONTFTRWVKNHLQKAG
ETIESLETDFSDGLKLIALAQVLSHKNVGKFNKKVAFRSQKLENVSLALNFFQNEENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKVAPLIAPAEMIHPEIDEMSVMTYLSQFPATKPIIMKPKVQATISNLDKILQVNDP
REFDLKLSRDGFKPKVSIRDEDGQDIHLSLKKVEDKENAYKVKFTPTKIGFIHVDVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDVHTFETQTIPBASVICQVVPIARLLDYNKTAKVGDDVKPAVVDAIEGPVEAIVVDP
TGKEHRMVILDGTSPGEHSFEYKIPCIGLHSVNVFHKKLPLTGSPFPLRGKPKNSFKV
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                                                                     complement(join(21251. .21978,22294. .22393,22461. .23015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Submitted by:
                                                                                                                                                                  /note="contains similarity to the 24 x 96 aa approximate repeats found in human filamin (BB:144140); coded for by the following C. elegans cDNAs: yk363412.5, yk348h4.3, yk33698.3, yk363412.3, yk356g8.5"
                                                                                            23696. .24231,24532. .24808,24850. .25412,25459. .25632,
26482. .26653,26702. .26815,26865. .26900))
/gene="Y66H1B.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Pred. No. 9.9;
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Caenorhabditis elegans cosmid T23B7, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
                                                                                                                                                                                                                                                                       /codon_start=1
/product="Hypothetical_protein_Y66H1B.3"
/protein_id="AAC69000.1"
/db_xref="G1:3801004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 17540 CAAGAAGATGTTATTGTGAAGAGAGACTCCTCTCTCAC 17502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of C. elegans cosmid T23B7
Unpublished (2001)
3 (bases 1 to 9056)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 16.2%; Score 33.4; D
1 Similarity 58.6%; Pred. No. 9.9;
58; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans
                                                 s=Sequence"
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Waterston, R.
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ACCESSION
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review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbi.nig.ac.ip/c-elegans/html/CE INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
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http://www.wormbase.org/db/seq/sequence?name=T23B7.1;class
                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein T23B7.1"
protein id="AAA91245.1"
/db xref="G1:121532"
/trānslation="WADKSAYWGAGGYGSGYMGSNASSSGYAREDYAQGGNGGGQQQQ
                                                                                                                                                       This sequence may not be the entire insert of this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.wormbase.org/db/seg/seguence?name=T23B7;class=Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The 5' cosmid is C33F10, 200 bp overlap; the 3' cosmid is F11G11, 200 bp overlap. Actual start of this cosmid is at base position 28965 of C33F10; actual end is at 12575 of F11G11.
                                                                                                                                                                                           It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coding seqences below are the result of integration and manual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1153. .1368
/gene="T23B7.1"
/note="coded for by the following C. elegans cDNAs:
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
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|db_xref="taxon:6239"
|chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             more than one m13 subclone.
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/gene="T23B7.1"
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                                                                                                                                                                                                                                                              neighboring submissions
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Gaps

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DB 3; Length 9056; 90; Indels

NQGSGGNTNPGGQVFKARTDQSCYLGP" 1738 c 1459 q 3120 t

1459 g

BASE COUNT

ORIGIN

2567 AATTATTTTCCGTTCCGACTCAAAATTAGATTAAATTCAATTACCAGCCTCCAGCATTTC 2626

28 AGTICITGGICAATITCCAGGACACAGATGATTCGGICCAAGAACAGGATAATAGAACTA 87

0; Mismatches Score 33; Pred. No.

87; Conservative

Matches

Pp δ

Department of Genetics, Washington University St. Louis , MO 63110, USA, and

Genome Sequencing Center

COMMENT

16.0%; 49.2%;

Query Match Best Local Similarity

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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                   HTG 13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 68850)
                                                             2627 AGCATTTTCCAAATTTGTTCCTTATTTTCCTTAAACTTGCTGACATCATTTTCGTAA 2686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATA 147
                                                                                                                                                                                     2687 CATTITICCAGIAAGAATCCCGGAAATCATAGCGAACAGIGAAAAATGTTACAGIGCT 2743
                                                                                                                                 148 GTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTATCCT 204
                                                                                                                                                                                                                                                                                                                                           ACULS6U6 68850 bp DNA linear HTG 13
Homo sapiens clone RP11-45E12, LOW-PASS SEQUENCE SAMPLING.
AC015606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888 987: gap of 100 bp
988 1854: contig of 867 bp in length
1855 1954: gap of 100 bp
1955 2812: contig of 858 bp in length
2813 2912: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                887: contig of 887 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-45E12
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HTG; HTGS PHASE0.
Homo sapiens.
Homo sapiens
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                               RESULT 18
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12499 12598: gap of 100 bp 12599 13465: contig of 867 bp in length 13565: gap of 100 bp 14466 13565: gap of 100 bp 1445 14544: gap of 100 bp in length 1445 14544: gap of 100 bp in length 14515 15514: gap of 100 bp in length 15515 16379: contig of 865 bp in length 15515 16379: contig of 865 bp in length
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contig of 869 bp in length
                     of 100 bp contig of 868 bp in length
                                                               of 100 bp contig of 861 bp in length
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contig of 867 bp in length
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                                                                                                                                                                                                                                                                                           4: gap of 100 bp
10550: contig of 866 bp in length
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10551 11522: contig of 872 bp in length
11523 11622: gap of 100 bp
11623 12498: contig of 876 bp in length
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16480 17344: contig of 865 bp in length
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18131 contig of 868 bp in length
1813 18412; gap of 100 bp
18413 19291; contig of 879 bp in length
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22202: cont
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74 38873: gap of 100 bp 3978: contig of 863 bp in length 397 gap of 100 bp 4070: contig of 864 bp in length 40700: contig of 864 bp in length 100 bp 
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of 863 bp in length
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57: contig of 865 bp in length
100 bp.
26: contig of 859 bp in length
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53302: contig of 875 bp
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/db_xref="taxon:9606"
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49406: contig
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68850: con+4
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50376: cont
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59105: cont
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63029: cont
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Query Match 16.0%; Score 33; DB 2; Length 68850;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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1 (Dases 1 to 99593)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Batbrooks, S. L., Amaratunge, H.C., Are, J.R., Pyele, M., Banks, T., Batbrooks, S. L., Amaratunge, H.C., Are, J.R., Brown, M., Bryant, N.P., Bunch, J., Burkett, C., Burch, P., Burkett, C., Burch, B. Brown, M. C., Carron, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chacko, J., Charez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Coyle, M. D., Dathorne, S. R., David, R., David, M.L., Dary-Carroll, L., Dederich, D.A., David, R., Ding, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhatt, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagan-Rocha, S., Hanmilton, K., Harris, C., Harris, K., Huber, J., Haves, A., Hernandez, J., Harris, K., Huber, J., Haves, A., Hernandez, J., Auber, J., Huber, J., Jacobson, B., Jai, Y., Johnson, R., Holloway, C., Hollins, B., Harris, C., Harris, K., Huber, J., Hugues, M., Holloway, C., Hollins, B., Harris, C., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loudsh, S., Loude, R., Ludia, Y., Johnson, R., Holloway, C., Hollins, B., Markenbin, S., Martin, R., Svacek, A., Rador, R., Sonch, R., Sonch, R., Sonch, R., Tamer, S., Scott, G., Shen, H., Shoshari, S., Rattus norvegicus clone CH230-267Pl1, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 43 unordered pieces.
AC127176
AC127176.1 G1:21747564
HTG 14-JUL-2002 Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, 17029 AGAAATGCTTACCTCGAGCACAGTAGGATTTACCAGAAAGCTACTGAGTCTAAACTCCAG 16970 16969 decentratricacadececentricaadececercadedeceaceradeaarenerala 16910 141 GTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTA 200 (bases 1 to 95983) (bases 1 to 95983) Rattus norvegicus Direct Submission Submission Unpublished Worley, K.C. Norway rat. Db 16909 T 16909 201 T 201 KEYWORDS SOURCE ORGANISM AC127176/c DEFINITION TITLE JOURNAL AUTHORS TITLE JOURNAL ACCESSION REFERENCE AUTHORS REFERENCE RESULT 19 VERSION g

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COMMENT

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Rattus norvegicus clone CH230-234D19, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
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/db_xref="taxon:10116"
/clone="(H230-267P11"
26462 a 19453 c 19249 g 25488 t
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NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                Sequencing vector: Jlasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 46755 bases at least Q40
Consensus quality: 53605 bases at least Q30
Consensus quality: 58794 bases at least Q20
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                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GQPZ
Center clone name: CH230-267P11
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Nature, D. Manan, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabbrooks S. L., Amaratunge, H. C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bries, M., Brach, E., Bryank, M. Branks, T., Barbay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavazo, D., Chen, G., Chen, R., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Deland, C.D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Deland, C.D., Denn, A.L., Ding, Y., Dinh, H.H., Deland, C.D., Edgar, D., Edwards, C.C., Elbaj, C., Bacctto, M., Barnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Earland, E., Howards, C., Harris, K.J., Forei, J., Foster, P. Frantz, P., Gorrell, J.H., Guevara, W., Gunaratne, P., Hales, S., Hamilton, K., Harris, K., Hart, M., Haves, A., Harnandez, O., Hodgson, M., Hogson, M., Holls, B., Harris, C., Harris, K., Hart, M., Haves, A., Jak, S., Gobbs, E., Harris, K., Hart, M., Haves, A., Jak, S., Judh, J., Kovar, C., Kratlovic, J., Kureshi, A., Loiner, S., Joudsh, S., Martinds, E., Martinda, E., Mitchell, T., Mohabbat, K., Morgan, M., Mana, J., Martinda, E., Mart
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Assembly program: Phrap; version 0.990329
Consensus quality: 94504 bases at least Q40
Consensus quality: 99249 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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----- Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GOHK
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TITLE
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COMMENT

## Consensus quality: 103736 bases at least Q20

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html). NOTE: This is a "working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. length bp in length in length bp in length length bp in length bp in length length bp in length length bp in length in length bp in length bp in length length bp in length of 1264 bp in length bp in length ength. ength ength length length ength ength length length length length ength ength length length length ength ength ength ength pp in ui dd contig of 1360 b gap of unknown l contig of 1681 b unknown ] of 1038 } 1207 of 1335 unknown of 1306 of 1458 unknown unknown of 1349 unknown 1255 unknown of 1296 unknown of 1048 1186 unknown unknown of 1279 of 1104 unknown 1250 1005 unknown of 1350 unknown of 1383 of 1302 unknown unknown unknown of 1342 unknown of 1228 unknown 1038 unknown of 1167 unknown 1131 unknown unknown unknown of 1140 unknown of 1057 unknown 1107 φ contig or gap of we gap of we gap of we contig or contig contig c contig c gap of c contig c contig gap of contig gap of contig 40180: 41961: 1048: 3550: 3650: 5045: 16249: 18746: 37134: :96667 21101: 21201: 31029: 32435: 33893: 33993: 35353: 35453: 38583: 38683: 40080: 11318: 3666: 3766: 5145: 16349: 18646: :96002 22651: 23858: 29633: 5092: 8744: 9951: 0051: 2549: 7489: 23958: 6420: 2449: 4992: 17589 26843 26844 28099 28199 29534 29634 30930 32336 32436 33894 33994 35354 35454 37235 38584 38684 40081 1049 11149 2413 35513 35513 3651 4993 65093 66421 7607 7707 7707 9952 110052 111219 112450 12450 12550 13767 13767 13767 15146 15146 17590 18647 18747 19997 20097 21102 21202 22552 23859 23959 25442 26744 7490

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AC090127 212404 bp DNA linear ROD 27-APR-2( Mus musculus chromosome 6, clone RP23-128D23, complete sequence. AC090127 AC090127.11 GI:20330898 Mus musculus. Mus musculus DEFINITION SOURCE. ORGANISM AC090127/c ACCESSION RESULT 21 KEYWORDS VERSION

linear ROD 27-APR-2002

Stren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Bactelen, V., Boguslavkiy, L., Boukhgalter, B., Brown, S., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzHugh, W., Gagae, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Jagos, B., Haaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kartasa, A., Lanceque, K., Landersares, R., Landers, T., Lahoczky, J., Levine, R., Lid, G., MacLean, C., Macdonald, P., Marquis, N., Meldrim, J., Mench, C., Norbu, C., Norman, C.H., McPherters, R., Meldrim, J., Mench, L., Norman, C.H., Phunkhang, P., Pierre, W., Pollara, V., Raymond, C., Retta, R., Rieback, M., Faley, R., Schuer, S., Schupback, R., Schauer, S., Schupback, R., Schauer, S., Schupback, R., Steanen, S., Schups, C., Retayer, J., Travers, M., Traylio, J., Vassiltev, H., Viel, R., Vo, A., Rilse, C., Submas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Submar, H., Suhmistre, A. and Zody, M., Shrhitter, M., Teffayer, Teffayer, Shrhitter, A., Shrhitter, S Birren, B., initon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Erom, A., Camarata, J., Campopiano, A., Chang, J.,
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Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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MacCarthy, M., McEwan, P., McKernan, K., Marquis, N., Marthews, C.,
Miova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Direct Submassion

AL Submitted (17-FBB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 21240,

Birren, B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,

Boukhgalter,B., Brown,A., Camarata,J., Campolano,A., Changalo,M., Collins,S., Collymore,A.,

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Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galdgan,J., Gardyna,S.,

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MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,

Oliver,J., Peterson,K., Phunkhang,P., Rise,C., Rogov,P.,

Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,

Saman,S., Severy,P., Spencer,B., Stange-Thomaman,N., Stojanovic,N.,

Yiel,R., Vo,A., Wilson,B., War,X., Wman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

AL Submitted (26-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Hirran B. Gardyna, S., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Birren, B., Linton, L., Nusbaum, C. and Lander, B. Mus musculus chromosome 6, clone RP23-128D23 (bases 1 to 212404) Unpublished TITLE JOURNAL REFERENCE JOURNAL REFERENCE REFERENCE JOURNAL REFERENCE AUTHORS TITLE TITLE

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24703. .24799
                                                                           14255. .14463
/rpt_family="L1"
complement(15279.
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:1111. .21130
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Soman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange, Thomann, M., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Zuinoun, J., Zembek, L., Zimmer, A., and Zody, M., Ye, W.J., Young, G., Direct Submission
                                                                                                                                           Submitted (27-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 26, 2002 this sequence version replaced gi:20219124. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                       .------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP23-128D23"
/clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9385. .9389)
/note="<30 qual SNGL region"
complement(9492. .9497)
/note="<30 qual SNGL region"</pre>
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complement(5509. .5795)
/rpt_family="Lx8"
complement(5799. .5851)
/rpt_family="Bl_MM"
7807. .7982
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complement (7995. .8272)
/rpt_family="MTD"
8281. .8302
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complement (3065. .3365)

/rpt_family="Lx8"

complement (4852. .5300)

/rpt_family="Lx8"
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/rpt_family="Lx8"
complement(9385. .9389)
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Center clone name: 128_D_23
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/chromosome="6"
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complement(528._.841)
/rpt_family="L1"
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3355. .8536
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rpt_family="AT_rich"
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12354. .12466
/rpt_family="(CA)n"
12467. .13522
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AC100386 213265 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP23-132J19, WORKING DRAFT SEQUENCE, 10
                                                                                                                                                                                                        76208 TAGATGGATCACAGTTCAAGGTTAACCTTCAATACAGAGGTAGTTTGAGGCTATCCTGGG 76149
                                                                                                                                                                                                                                                                                                                                       76148 TTAATGAGACTCTGTCACATGAGAGAGAGAGTGTGAAATCCACTGAAACCACATGGAACT 76089
                                                                                                                                                                                                                                                                         76 ATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACT 135
                                                                           Gaps
                                                                                                                                      16 TGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGG
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0
Score 33; DB 10; Length 212404;
Pred. No. 14;
0; Mismatches 70; Indels 0;
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AC100386.3 GI:2238146
HTG; HTGS_PHASE1; HTGS_FULLTOP.
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KEYWORDS
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TITLE

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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                     Insert sizē: 212365; sum-of-contigs
Quality coverage: 11.4 in Q20 bases; sum-of-contigs
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Consensus quality: 211773 bases at least Q30 Consensus quality: 212130 bases at least Q20
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150254. .213265
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                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Bouckhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazoro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Karatas, A., Karatas, A., Karatas, A., Karatas, M., Melhecters, R., Meldrim, J., MacLean, C., Macdonald, P., Major, J., Merquis, N., Mathaws, C., Macdonald, P., Major, J., Merquis, N., Mathaws, C., Maccan, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Siley, R., Schauer, S., Schupback, Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Millon, M., Willen, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Mallen, M., Millon, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Mallen, M., Man, M., Wyman, D., Ye, Wallen, Y., Woller, S., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Man, M., Willen, M., Wallen, M., Wallen, M., Willen, M., Willen, M., Wyman, D., Ye, W.J., Young, G., Man, M., Wallen, W., Wallen, M., Wallen, M., Wallen, W., Wallen, W.,
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Submitted (12-NOV-2010) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 211265)

Birren, B., Wusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faron, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Crand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Lohnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Jones, C., Kamat, A., Maclan, J., Maylor, J., Naylor, J., Mitova, T., Mitova, T., Mitowa, T., Mitowa, T., Mitowa, T., Mitowa, T., Mitowa, T., Norman, C., Phunkhang, P., Pierre, W., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tepfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vo, A., Wilso, D., Topham, K., Travers, M., Vassiliev, H., Vo, A., Wilso, D., Topham, K., Travers, M., Vassiliev, H., Vo, A., Wilso, D., Will, M.X., Wyman, D., Young, G., Zainoun, J., Vol, A., Wilso, D., Will, W.X., Wyman, D., Young, G., Zainoun, J., Now, S., Will, M.X., Wyman, D., Young, G., Zainoun, J., Now, J., Topham, W.X., Wyman, D., Young, G., Zainoun, J., Kltp, Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:html
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 213265)
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Center: Whitehead Institute/ MIT Center for Genome Research
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------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.9660731
Consensus quality: 210877 bases at least Q40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                       Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-132J19
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                                                   Mus musculus
                                                                                                                                                                                                                                                                                                 Unpublished
                                              ORGANISM
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AUTHORS
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Db 125005 TCATACTCAATTCAGACTTTAGTGTGTGTTCCATTCCTAAAACAAGACAAAAGGGGGGAAC 125064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.0%; Score 33; DB 2; Length 213265; 54.5%; Pred. No. 14;
                                                                                                                                                                                                                                                  116950 117049: gap of 100 bp 117049: 117050 150153: contrig of 33104 bp in length 117050 150253: gap of 100 bp 100 bp 150254 213265: contrig of 63012 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 others
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                                                                                                                       59879 59978: gap of 100 bp
59979 88828: contig of 28850 bp in length
                                                                                                                                                                                      88829 88928: gap of 100 bp
88929 116949: contig of 28021 bp in length
                                                               41072: gap of 100 bp 59878: contig of 18806 bp in length
31773 31872: gap of 100 bp 31873 40972: contig of 9100 bp in length
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COMMENT

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gene CDS

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molecules: Protein, peptide secretion"

Those="Residues" 5 to 150 of 150 are 44.52 pct identical to residues 5 to 150 of 263 from GenPept 118 :

gi|404292|emb|CAA51926.1| (X73525) surface presentation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MGEVILYQLHSLLAATALGFCRLAPTFYLLDFFASGNIPTVVRH
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DNQRGATLSSTLDPATGVDTSELARLFNLFSAAVYLTNGGLNFILETL"
                                                                                                                                                                                                                                                                                                              BCT 21-MAR-2001
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/note="O-island #115; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
complement(70. .522)
                                                                                                                                                                                                                                                                                                           AE005515 10875 bp DNA linear BCT 21-MAR-2001
Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 134
                                                  Db 125065 AACACATTACAATTTTATAGTAATGTTCTTCTTATAACAGTAAATAAGAAGTTCAAAATC 125124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 10875)
Perna, NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Maybew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Agodeck, B.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 10875)
Pernah, NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Aposfai, G., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
91 AACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGTCCATAGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (22-OCT-2000) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="Z4187"
function="putative transport; Transport of large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
trans1_table=11
/produc2="type all secretion apparatus protein"
/protein_id="AAG57979.1"
/db_xref="GI:12517365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Escherichia coli 0157:H7 EDL933"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli O157:H7 EDL933.
Escherichia coli O157:H7 EDL933
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AE005515.1 GI:12517364
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KEYWORDS
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Translation="MKANSKTIRRMKVNVRSEBSKSKHSTFETTFQNWKENGEDVALL
MPEFBAKWLDIAEEGSSWSGWVLLREIFPLISAELAGMALMPETERLIGEWLSLSSSP
LINLKYPELKYNRLCVGKYFDGVLSPOPLIR INTGELNLWLDKVTVCQYENAPTLDKK
SLYWPIHFYGRSKTYCYRTVDIEVGDVLISNNMAYAVINTKIOLIYPEELKMAD
HFQYEBDFETDDFDIKKSESEIYDENDEQMINSFEELPVKIEFVLGKKINNLYEIDEL
CAKRIISLLPESEKNIEIRNGALTGYGELVEVDDKLGVEIHSWLSGHNNVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules: Frotein, peptide secretion"
/note="Residues 1 to 218 of 221 are 69.05 pct identical to essidues 1 to 223 of 224 from GenPept 118 :
gi|975759|gb|AAC43849.1| (U29360) SpaP [Salmonella enterica]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTSRDQSINSELSNRTIQFKEKIHNGIHTEYITDQKHSNNKDRE
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QTLPFGVKLLCVSICFPLMSGWYGSKLYSFGIEMLNLAFARG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVESIMTLINGVALLLISMFVMMPVGKEITYNSONENLEFNNVASVVNFVETGMSGYKSY
LIKYSEPELVSFFEKIQKVNSSEDNEEIIDDDNISIFSLLPAYALSEIKSAFIIGFYI
YLPFVVVDLVISSVLLTLGMMMMSPVTISTPIKLILFVAMDGWTMLSKGLILQYFDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MSNSISLIAILSLFTLLPFIIASGTCFIKFSIVFVIVRNALGLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/product="putative integral membrane protein-component of
typeIII secretion apparatus"
/protein_id="AAG57981.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="putative transport; Transport of large molecules: Protein, peptide secretion"
/note="Residues 35 to 326 of 328 are 32.44 pct identical to residues 23 to 301 of 303 from GenPept 118 : gi|973281|gb|AAC43947.1| (U29351) SpaO [Salmonella enterica]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules: Protein, peptide serretion"
/note="Residues 97 to 178 of 189 are 38.55 pct identical
to residues 252 to 332 of 336 from GenPept 118 :
gi|1155301|gb|AAC45001.1| (U43305) SpaN [Salmonella
                       /function="putative transport; Transport of large molecules: Protein, peptide secretion"
//note="Residues 1 to 86 of 86 are 68.60 pct identical to residues 1 to 86 of 86 from GenPept 118 :
gi|273263|gb|AAC43967.1| (U29346) SpaQ [Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="putative transport; Transport of large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="putative transport; Transport of large
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/product==type III secretion apparatus protein"
/protein id="MAG5983.1"
/b_xrefe="GI:12517369"
                                                                                                                                                                                                                /transI_table=11
/producg="typeIII secretion apparatus protein"
/protein id="MAG57982.1"
/db_xrefE="GI:12517368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (1450. .2436)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (795. .1460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="GI:12517367"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (795. .1460)
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gene="Z4188"
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Best Local Similarity
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                                                                                                                                                                  /codon start=1
/transl_table=11
/product="orf; hypothetical protein"
/protein_id="AAG57984.1"
/db xref="01:12517370"
/translation="MDEVKXIEHCKILNTDTPDNSASDLDSFLKKNKKNKEMSEIVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ransT_table=11
/product="type III secretion apparatus protein"
/protein_id="AA657986.1"
/brotein_id="AA657986.1"
/db_xref="G1.12517372"
/db_xref="G1.12517372"
/translation="MSCDMEHAGMKKIKLINKYSYLHSINGSLIEBELDDVSVGEVCE
IYASRQAMERIARAQVVGFRNGKTLINLIGSSVGLTRTAVLKPTGEDLITQISDAFLG
SVLNASGQIMBREVPOTPGDRGNLRILIDELPSYQBRRVINTPLETRIRVIDGVLTCG
IGQRVGIFASAGCGKTVLMHMLVNNTEADVFVIGLIGERGREVTECAESLKKSVNAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                molecules: Protein, peptide secretion"

Those="Residues 2" to 102 of 111 are 31.68 pct identical to residues 45 to 145 of 147 from GenPept 118 :

gi|l155297|gb|AAC44998.1| (U43304) SpAM [Salmonella
VRENELTYQFQRWGQNHTVRILESSEGIRLKPSDTLVSDRLHEAQHNDVTAQRWVLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MQLKNLQSLLDMKELLGEVVFRQDIFYSLRKVTVIQQQIAEINL
EKQKIAERRKILNKEIVQQQAQRKHWWLKGEKYDRLKKRIKKQLLNQMLYQDELEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVLVYATSDFSSVDRCNAALMATTVAEYFRDRGKRVVLFIDSWTRYARALRDMKLAAG
BPARRGYPAASVFDSLPRLLERRGFTLKGSTTFFYTVLLEGEDBSDPLGDEIRSLIDG
HIYLSRKLAQQGHYBIDULKSVRYBYGQVTDEKHRDNAARVRKNLTTLEDLQVFIDL
GEYRAGQNAENDFAMNARPKLTNWLKQSVNEKMGRENERILKELERIVK"
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Thote="Residues 1 to 686 of 686 are 64:00 pct identical to residues 1 to 685 of 685 from GenPept 118 :
gi|461369|gb|AAA16867.1| (M90846) GTG start codon
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//note="Residues 10 to 396 of 439 are 63.30 pct identical to residues 1 to 386 of 432 from GanPept 118 ;
gi | 497222 | gb | AAA74038.1 | (U08279) invC (Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative transport; Transport of large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Z4195"
/function="putative transport; Transport of large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
/product="type ll secretion apparatus protein"
/protein_id="AAG5'985.1"
/db_xref="GI:12517371"
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                                                                                                                           'Éunction="orf; Unknown function"
                        QDERQGQRHQPHEEQENEGKFENDQKDES"
complement (3038. .3271)
                                                                                                                                                  'note="No significant matches"
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                                                                              complement (3038. .3271)
/gene="Z4192"
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complement (3697. .5016)
/gene="Z4194"
                                                                                                                                                                                                                                                                                                                           complement (3249. .3584)
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                                                                                                                                                                                                                                                                                                                                                                                          /gene="Z4193"
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                                                                 /gene="Z4192
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Birren, B., Linteon, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-141E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13213 TGGCCAATTTTCTGGACGGAGAATATGTCCTGGAAGACCAGCCAATAGAAAAACGG 13154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13153 ACAAAGTTATGGAĞGCĞCTTAAĞGCTGCAAĞTAĞĞCTĞAĞTÇATGAAĞTGTATAĞCTTTG 13094
                                                           7942 ACAAAGTTATGGAGGCGCTTAAGGCTGCAACTACCCATGACTATGAAGTGTATAGCTTTG 7883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner,F.R., Burland,V., Perna,N.T., Plunkett,G. and Welch,R. Sequences of B. coli 0157
Patent: US 6365723-4 166 02-APR-2002;
Location/Qualifiers
94 GCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTT 153
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Mus musculus clone RP24-141E2, LOW-PASS SEQUENCE SAMPLING.
AC108788
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                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                         7882 CTAAAAATTATTCCCAGATGAAAGCGATCTGGTAGTTGTGTTA 7839
                                                                                                                                  154 CACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGTTA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 CACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
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                                                                                                                                                                                                                                                                                                                                                                                           DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 166 from patent US 6365723.
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50.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                           16950 bp
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3505 c 2750 a
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Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Comnor, P., Nguyen, C., Nicol, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (31-JAM-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Bitren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Buckhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colanglo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hangos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landerse, R., Landers, T., Lehoczky, C., Merquis, N., Marchews, C., McCarthy, M., Major, J., Marquis, N., Marchews, C., McCarthy, M., Major, J., Marquis, N., Mardul, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Sahce, S., Schuuch, S., Schuck, S., Schuuch, C., Travere, M., Travis, N., Trigilio, J., Vashiley, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUN 14, 2002 this sequence version replaced gi:18450046. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
------- Genome Center
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------ Project Information
Center project name: 1.19501
Center clone name: 141_E_2
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Web site: http://www-seg.wi.mit.edu
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17694 18556: gap of 100 bp 18557 18556: gap of 100 bp 19435 19334: contig of 763 bp in length 19457 18556: gap of 100 bp 19435 19434: gap of 100 bp 19435 20207: contig of 773 bp in length 20208 20307: gap of 100 bp 20308 20305: gap of 100 bp 20306 22765: contig of 770 bp in length 20306 2265: gap of 100 bp 20308 23579: contig of 732 bp in length 20308 23579: contig of 732 bp in length 20308 23579: contig of 732 bp in length 20308 23579: contig of 730 bp in length 20308 23579: contig of 750 bp in length 20308 20309: contig of 764 bp in length 20308 23579: contig of 765 bp in length 20309: contig of 764 bp in length 20309: contig of 764 bp in length 20309: contig of 767 bp in length 203008: contig of 767 bp in lengt
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33007 33718: contig of 712 bp in length
33719 33818: gap of 100 bp
33819 34558: contig of 740 bp in length
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f 735 bp in length
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17593: contig of 766 bp in length
contig of 672 bp in length
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78: gap of 100 bp
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5763
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Homo sapiens PAC clone RP5-999D10 from 7, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           39522 39721: Gap of 100 bp 101 bp 101
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The sequence of Homo sapiens PAC clone RP5-999D10
Unpublished
34559 34658: gap of 100 bp
34659 35420: contig of 762 bp in length
35421 35520: gap of 100 bp
35521 36279: contig of 759 bp in length
                                                                                                                                                                                                                                                                                                    56: gap of 100 bp 18820: contig of 764 bp in length 20: gap of 100 bp in length 39621: contig of 701 bp in length
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47349: contig of 764 bp in length
                                                                                                                                                      p of 100 bp contig of 738 bp in length
                                                                                                                                                                                                                                 17: gap of 100 bp
37956: contig of 739 bp in length
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1 (bases 1 to 90422)
Sulston, J.E. and Waterston, R.
                                                                                                                                                  36280 36379; gap of 36380 37117; cont 37118 37217; gap of
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AC023880.5 GI:11597112
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Waterston, R.H.
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This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                 MO 63108, USA
4 (Dases 1 to 90422)
Waterston, R.H.
Direct Submission
Submitted (07-DEC-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.hhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-658N17. Actual start of
this clone is at base position 1 of RP5-999D10; actual end is at
base position 90422 of RP5-999D10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAY-2001) Department of Genetics, Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Waterston, R.H.
Direct Submission
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Waterston, R.
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Page 31

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 131133)
Waterston,R.H.
                                                                      EST H68877 (NID:g1030440) yr93f12.rl"
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Center code: WIGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
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18521 ...18605
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Waterston, R.H.
Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                  contig of 10876 bp in length contig of 10876 bp in length contig of 9267 bp in length gap of unknown length length of 10876 bp in length contig of 14012 bp in length contig of 17041 bp in length gap of unknown length contig of 17207 bp in length gap of unknown length contig of 1836 bp in length gap of unknown length contig of 1636 bp in length contig of 1649 bp in length contig of 1649 bp in length gap of unknown length contig of 1649 bp in length contig of 1649 bp in length lengt
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gap of unknown length
contig of 4061 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
bp in length
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8968. .12623
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/note="assembly_name:Contig12"
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gap of unknown 1
contig of 7443 b
gap of unknown 1
contig of 7264 b
gap of unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 1860 b
gap of unknown l
contig of 2836 b
gap of unknown l
contig of 1771 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown of 9511 h
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gap of unknown
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gap of unknown
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/organism="Homo sapiens"
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ACO21843 159480 bp DNA linear PRI 01-MAY-2001
Homo sapiens chromosome 18, clone RP11-713C1, complete sequence.
ACO21843
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%; Score 32.6; DB 2; Length 131133; 57.3%; Pred. No. 19; tive 0; Mismatches 44; Indels 0;
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-713C1
Unpublished
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                     'note="assembly_name:Contig13"
                                                           /note="assembly_name:Contig14"
                                                                                                                                                   /note="assembly_name:Contig16"
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127361. 131133
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116745. .118393
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118494. .120493_
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120594. .122453
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122554. .125389-
/note="assembly_name:Contig7"
125490. .127260
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115009. .116644
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Direct Submission

Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 159480)

Birran,N., Bastien,V., Boguslarkiy,L., Boukhgalter,B., Brown,A., Camaraca,J., Campopiano,A., Chong,V., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Govette,M., Graham,L., Gardyna,S., Ginde,S., Govette,M., Graham,L., Gardyna,S., Ginde,S., Govette,M., Graham,L., Grand,D., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Maccarthy,M., Macclean,C., Macdonald,R., Marquis,N., Matthews,C., McCarthy,M., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norwan,D., McKernan,K., McPheteres,R., Meldrim,J., Mencus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Rostaus,M., Stance,R., Schauer,S., Schupback,R., Seaman,S., Schoper,C., Travers,M., Travers
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacGanald, P., Marguis, N., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mornow, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wuxx, Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Viel, R., Vo, A., Wuxx, Wyman, D., Ye, W.J., Zimmer, A., and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-713C1"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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complement(4703..5006)
/rpt_family="Alux"
50977..5439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(TG)n"
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complement(2960. .3097)
/rpt_family="L2"
3071. .3385
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/chromosome="18"
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/rpt_family="(TG)n"
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32082. .3210
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?5292. .27905
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34694. .3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MLT1K"
complement(35073. .35155)
                                                                                                                                                                                                                                                                                             omplement (16391. .16722) rpt family="L3"
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.8985. .19022
                                                                                                                                                                                                                                                                                                                           omplement (17184. .17371)
                                                                                                                                                                                                                                                                                                                                                      omplement(17373. .17582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MER4A-int"
24860. .24985
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complement(24986, 2529;
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/rpt family="AluSx"
complement (8459. .8997)
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complement(24013..2414
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complement(32777. .328
                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
9856. .20163
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/rpt_family="ERVL"
11251. .11376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21258. .21607
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21610. .24012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MER4A"
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1258. .21607
                                                                                                                                                                                                                           rpt family="MER5B"
1796. .12151
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29579. .29695
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                                                                                                       'rpt_family="ERVL"
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                                                                                                                                                                                                                                                                                                                                                                      family="L3"
                                                                                                                                                                                                           complement (11398
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Homo sapiens chromosome 18 clone RP11-82109 map 18, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 168406)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-82109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 TAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 CGAGTICTIGGICAATITCCAGGACACAGATGATICGGICCAAGAACAGGAIAATAGAAC 85
                                                                                                                                                                                                                                                                              76556. 36957
/note="1329 bp of Th10 sequence in BAC removed from submission"
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.8%; Score 32.6; DE
51.7%; Pred. No. 19;
Live 0; Mismatches
                                                                                                                                  /rpt_family="(TA)n"
complement(35965. 36278)
/rpt_family="L2"
36390. 36428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="MLT1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (40994. .41334)
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                  complement (35189. .35359)
                                                complement (35388. .35489)
                                                                                                                                                                                                                          /rpt_family="AT_rich"
complement(36429..36740)
/rpt_family="MER2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (42570. .42863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family=" (TTCA)n"
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39240, .39807
                                                                                              /rpt_family="MER58A"
35767. .35860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80465 AATCTGTGAAGAACAATTCCAAG 80443
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complement(40110.
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8652. 39221
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                                                                                                                                                                                                                                                                                                                                          .37356
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Best Local Similarity 51.7%;
Marches 74; Conservative
                                                                                                                                                                                                                                                                                                                                          37166.
                                                                          'rpt_fe
15490.
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Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Headrod, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocton, E., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocton, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macchan, C., Macchand, P., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Maren, C.H., O'Connor, T., O'Connor, T., Mlenga, V., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Schupback, R., Senery, P., Schupback, R., Schauer, S., Schupback, R., Schauer, S., Schupback, R., Schauer, S., Schupback, R., Senery, P., Travers, M., Tarvis, N., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zod, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 23, 2001 this sequence version replaced gi:13270639. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.960731
Consensus quality: 165824 bases at least Q40
Consensus quality: 166641 bases at least Q30
Consensus quality: 167254 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 188006; sum-of-contigs
Quality coverage: 10.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22614 56584: contra of 100 bp
56585 56684: gap of 100 bp
56685 168406: contra of 111722 bp in length.
Location/Qualifiers
1. 168406
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1. .5990
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6091. 13492
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/note="assembly_fragment"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 170337)
1. Hattori,M., Ishii,K., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 170,337 genomic DNA of 18q21
1. (Dases 1 to 170337)
1. Lases 1 to 170337
1. Ada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 170,337 genomic DNA of 18q21
1. (Dases 1 to 170337)
1. Ada,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
1. Submitted (09-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1. 15. 1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Jul 14, 2000 this sequence version replaced gi:8307703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170337 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 18 clone RP11-82109 map 18q21, WORKING
AP001378
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                                                                                                                                                                                                                                                                                                                                                                                         86 TAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAACTTCCTGTGACTAACAGGTCCA 145
                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                  26 CGAGTICITGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAAC 85
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                                                                                                                                                                                                                                                            DB 2; Length 168406;
                                                                                                                                                                                            400 others
                                                                                                                                                                                                                                                                                                       69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------- Project Information
                                                                                                                                                                        ecto<u>r</u> side:right"
3290<u>3</u> c 33972 g 49435 t
                                                                                                                                                                                                                                                                                Pred. No. 19;
0; Mismatches
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Center clone name: RP11-82109
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-82109.
                    13593. .22513
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                                                      22614. .56584
/note="assembly_fragment"
/note="assembly_fragment"
                                                                                                      56685. 168406
/note="assembly_fragment
                                                                                                                                                                                                                                                            Score 32.6;
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51.7%;
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Matches 74; Conservative
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AUTHORS
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KEYWORDS
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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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155304. .160993
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                                                                                                                                                                                     50774 bp in length 23667 bp in length 24352 bp in length 23721 bp in length 1155 bp in length 11155 bp in length 5429 bp in length 5690 bp in length 3298 bp in length 1030 bp in length
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50875 74541: contig of 23667 bp in length
74542 74641: gap of 100 bp
74642 98996: contig of 24355 bp in length
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99097 122817: contig of 23721 bp in length
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122918 138419: contig of 15502 bp in length
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169308 170337: contig of 1030 bp in length.
Location/Qualifiers
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99097. .122817
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122918. .138419
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138520. .149674
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149775. .155203
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/db_xref="taxon:9606"
/chromosome="18"
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repeat region
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Also Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles, Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                               26 CGAGTICTIGGICAATITICCAGGACACAGATGATICGGTCCAAGAACAGGATAATAGAAC 85
                                                                                                                                                                                          Query Match
Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0;
                                                                                                               1000 others
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165910. .169207
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Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Santos, K., Schauer, S., Schupback, R., Schamer, S., Schupback, R., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Yabacer, M., Travis, N., Traigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Librect Submission

Librect Submission
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complement(783. .827)
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1. .170843
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ement()
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family="L2"
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746<u>5</u>.
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All Unpublished

Interest Submission

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AL Submitted (12-000) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

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3 (bases 1 to 176562)

4 (bases 1 to 176562)

5 (Staul, R. K., Olson, M. V., Zhou, Y., James, R. A., Raymond, C.,

Clendenning, J., Ivey, R.G. and Haugen, E.D.

Direct Submission

AL Submitted (19-Apr.-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

4 (bases 1 to 176562)

5 Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K. A., Raymond, C. and Haugen, E.D.

Direct Submission

AL Submitted (10-Apr.-2002) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

5 (bases 1 to 176562)

5 Kaul, R. K., Olson, W. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E. D.

Direct Submission

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC084864 176562 bp DNA linear PRI 26-MAY-2002
Homo sapiens chromosome 7 clone RP11-738B7, complete seguence.
AC084864
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Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                   Db 132779 TCCATGAGTCTATACAGATATAGATGATTTTAAAAATAATAATTGGAGTAAAAGGGACA 132838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176562)
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                                                                                                                                                                                                                                                                                                                                                                                                                          86 TAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCA 145
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                  26 CGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAAC 85
                                                                                                                                                                                                                Length 170843;
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Center Code: UWGC
                                                                                                                                                                                                                                                              69; Indels
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Contact: uwgchtgs@u.washington.edu
------ Project Information
                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                       Query Match
15.8%; Score 32.6; DE
Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches
                                                                            /rpt_family="LiM4c"
20522. .20618
/rpt_family="FLAM_A"
20619. .20693
                     /rpt_family="MIR"
20296. .20517
/rpt_family="L1M4c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 132839 AATCTGTGAAGAACAATTCCAAG 132861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 TAGTTTTTCACGACACTTCCAAG 168
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19504.
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7824         8087         1345         1347         1474           1721         1744         2481         2480         2724           313         <800         2806         2809         12250           0245         10620         594         <800         8808           2957         2902         1091         1115         3945           4167         4235         1129         1115         4649           6118         6170         2198         2282         1854	2065 24114 24615 265 24114 24615 24816 24846 2477 2480 110620 1254 1273 77 6800 1397 1507 17 6800 23724 3797 28	3373	22 <800 5265
		Tri G	5639 2056 6222 <800 16959 4079 6481 <800 2559 <800 21902 Source 3411
Center project name: chr-7  Center clone name: RP11-738B7 (djs722)  Assembly program: Phrap; version 0.990319  Consensus quality: 176414 bases at least Q40  Consensus quality: 176547 bases at least Q30  Consensus quality: 176562 bases at least Q20  Insert size: 176562; sum-of-contigs  Quality coverage: 12.0x in Q20 bases; sum-of-contigs  Overlapping Sequences:  S:: RP11-448419 (UWGC:djs705) AC078846 58194-bp overlapp 3': RP11-437L1 (UWGC:djs723) AC084865 98271-bp overlap	e quality regram. I to quality we less than lly visible as part s otherwise sequenced wi lity data (1. live all sequence all regions more than or	Sequence Validation:  Sequence Validation:  Sequence Validation:  This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.  The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.  ECORI  Hindli  SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	9894 9869 5769 6382 6431 2067 449 <800 135 22215 21921 17291 14723 14460 4160 300 <800 89 2525 580 5255 3459 3373 681 2272 2282 3456

<800 <800 <800 <800 <800 

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AC096176.3 GI:21723315
HTG; HTGS_PHASE1.
Norway rat.
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171153:
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166856:
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155756:
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    be preserved
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AC096176
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Submitted (18-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jan 14, 2001 this sequence version replaced gi:9690421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC073474 1176715 bp DNA linear HTG 14-JAN-2001
Homo sapiens chromosome 7 clone RP11-658N17, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 176715) Waterston, R.H.
                                                                                                                                                                                                                                                                                                              Db 145556 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 145497
                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                          19 ACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATA 78
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                                                                                                                                                                                    Length 176562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project Information
Center project name: H NH6658N17
Sequencing vector: M13, 68%
Sequencing vector: plasmid; 33%
Chemistry: Dye-primer ET; 68% of reads
Chemistry: Dye-terminator Big Dye; 32% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 171198 bases at least Q40
Consensus quality: 172484 bases at least Q20
Consensus quality: 173217 bases at least Q20
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Insert size: 175815; sum-of-contigs
Quality coverage: 5.81 in Q20 bases; agarose-fp
Quality coverage: 6.54 in Q20 bases; sum-of-contigs
                                                                                                                                                                                      Query Match 15.8%; Score 32.6; DB 9; Length 1
Best Local Similarity 57.3%; Pred. No. 19;
Matches 59; Conservative 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
Web site:http://genome.wugtl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                              Db 145496 Grgcaggaaaacaagaaagaaarrirrcagagraracrcaaaa 145454
/clone="RP11-738B7"
/clone lib="RPCI human BAC library 11"
47363 - 47572
/standard_name="SWSS3347"
                                                                                                                                                                                                                                                                                                                                                         79 ATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC073474.3 GI:12225355
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
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                                                                               56730. .56808
/standard name="sWSS3322"
121881. .122003
/standard_name="sWSS4084"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Homo sapiens clone Unpublished
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
AC073474/c
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ACO96176 177013 bp DNA linear HTG 11-JUL-2002 Rattus norvegicus clone CH230-11D3, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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4: contig of 20174 bp in length
6: gap of unknown length
6: gap of unknown length
6: gap of unknown length
6: contig of 49750 bp in length
6: gap of unknown length
7: contig of 2022 bp in length
7: contig of 2022 bp in length
7: gap of unknown length
8: contig of 2899 bp in length
6: gap of unknown length
8: contig of 1990 bp in length
9: gap of unknown length
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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/note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20275. .43776 // note="assembly_name:Contigll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43877. .93626 // note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig13"
149076. .151077
/note="assembly_name:Contig4"
151178. .152757
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152858. .155756
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155857. 166756
/note="assembly_name:Contig9"
166857. 171053
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49104 a 39617 c 39214 g 47873 t
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171154. .176715
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/chromosome="7"
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Muzny, D.M., Adama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albbrooks, S.L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Barbaraia, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Brabbrooks, S.L., Amaratunge, H.C., Buren, E., Bryank, M. Barks, T., Barbaroks, S.L., Brieva, M., Brown, E., Bryank, N.C., Chavez, D., Carron, T.E., Carron, F.E., Burch, E., Burch, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chavez, D., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Deladand, C.D., Cox. C., Coyle, M.D., Dathorne, S.R., David, R., Deladand, C.D., Cox. C., Coyle, M.D., Dathorne, S.R., David, R., Deladand, C.D., Danste, C., Elbaj, C., Bearich, D.A., Bearich, D.A., Bearich, D.A., Garcia, A., Garrer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Qunaratne, P., Hale, S., Hamilton, K., Barnhart, C., Bagar, D., Edward, C.C., Elbaj, C., Barch, C., Haring, K., Harr, M., Havring, R., Harrandez, C., Harris, K., Harr, M., Havring, R., Harrandez, C., Harris, K., Harr, M., Havrlak, P., Hawes, A., Harnandez, C., Harris, K., Harr, M., Havring, M., Gorrell, J., Gorson, B., Gorson, R., Hollies, M., Gulivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovrah, J., Kovar, C., Kraebni, A., Martin, R., Martin, M., Loal, B., Martin, R., Martin, M., Lai, B., Martin, R., Martin, M., Mapus, P., Martin, R., Martin, M., Mapus, P., Martin, R., Martin, M., Mapus, P., Marken, M., Martin, M., Martin, M., Mapus, P., Marken, M., Nickerson, E., Marken, M., Pat, C., Luna, K., Martin, M., Mapus, P., Marken, M., Shooshtari, N., Sison, I., Scherer, S., Scott, G., Marte, R., Washington, C., Wallinson, A., Wallinson, A., Waller, M., Wall, M., Y.F., Tansey, J., Taylor, C., Taylor, T., Telirod, B., Tamerisa, N., Tansey, J., Taylor, C
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Direct Submission
Submitted (17-SE201) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 177013)
Worley, K.C.
Worley, K.C.
Worley, A.C.
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                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113564 bases at least Q40
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GEOZ
Center clone name: CH230-11D3
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/doss/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 73 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 120262 bases at least Q30 Consensus quality: 127025 bases at least Q20
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens

ORGANISM

AUTHORS

1 (bases 1 to 214162) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D. Direct Submission

Submitted (23-NOV-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA (bases 1 to 214162)

(bases 1 to 214162) 1,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.

Kaul, R., Olson, M.V Direct Submission

JOURNAL

TITLE

AUTHORS

Unpublished

JOURNAL

TITLE

Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C., Clendenning,J., Ivey,R.G. and Haugen,E.D. Direct Submission Submitted (01-MAY-2001) Genome Center, University of Washington,

TITLE JOURNAL

AUTHORS

Dec 352145, Seattle, WA 98195, USA

(Dases 1 to 214162)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, G., Phelps, K.A., Raymond, C. and Haugen, E.D.

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Direct Submission Submitted (06-APR-2002) Genome Center, University of Washington, Box 352185, Seattle, WA 98195, USA On Apr 6, 2002 this sequence version replaced gi:13899421.

JOURNAL

TITLE

AUTHORS

Center: University of Washington Genome Center

Web site: http://www.genome.washington.edu

Center Code: UWGC

Contact: uwgchtgs@u.washington.edu

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RP11-738B7 (UWGC:djs722) AC084864 98271-bp clone overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compression repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                Quality coverage: 9.9x in Q20 bases; sum-of-contigs
                                                                            Assembly program: Phrap; version 0.990319
Consensus quality: 213991 bases at least Q40
Consensus quality: 214149 bases at least Q20
Consensus quality: 214162 bases at least Q20
                                      Center clone name: RP11-437L1 (djs723)
                                                                                                                                                                                                                                                                                          Insert size: 214162; sum-of-contigs
Center project name: chr-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3': Mapping in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                     Overlapping Sequences:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Validation:
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies

PRI 06-APR-2002

AC084865.3 GI:20066285

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

LOCUS

Homo sapiens

4175 2334 2307 3878	2956 2951 910 470 <800 7 <800 6414 6405 34 <800	454 <800 912	22 <800 3434 3705	3821 3793 5265 5138	20519 20664 81 <800	9726 10019 327 <800	777 787 2986 3002	310 <800 1038 1035	2806 2798 5200 5138		1272 1256 2714 2754	3793 684	1397 1411 2611 2754	7806 17895		2478 7997	1	920 912	19 <800	FEATURES Location/Qualifiers source 1214162	/organism="Homo sapiens" /db xref="Laxon:9606"		Query macch 15.8%; Score 32.6; DB 9; Length 214162; Best Local Similarity 57.3%; Pred. No. 19; Marches 59; Conservative 0: Mismarches 44: Indels 0: Cans 0:	の		らったもの。これらいないではない、これではないないないであっているというないないないないないないないないないないである。これではないないないないないないないないないないないないないないないないないないない	A AINGAMULANGCAAIGGGAIACAAIIIGGGIGGAIIIGGGAAGAA	DD 67205 GIGCAGGAAAACAAGAAGAATAITIICAGAGIATAGICAAAA 67163	RESULT 36	AC005872 AC005872 89672 bp DNA linear PRI 02-MAR-1999	Homo sapiens chromosome 10 clone sequence.	ACCESSION AC005872 VERSION AC005872.2 GI:4314335	
y ordered I	FngrPrnt	5785	2040	7259	3002	6289	10586	3705	<800	4824	12611	3914	<800	3914	5138	12611	9149	14245	3532	<800	3267	<800	<800	2571	802	3914	4824	<800	6795	3267	3002	1830	8060
between the experimental and predicted values. Uniquely fragments are separated by dashed lines. ECORI	SeqDerMap	5843	2067	7141	2876	6256	10615	3497	159	4753	12829	3637	120	3679	4936	12812	9178	14447	3359	238	3135	77	453	2581	802	4013	4794	598	6867	3024	2821	1863	8043
edicted val ed lines. III	FngrPrnt	5506	6405	<800	×800	11201	6952	1613	18849	3793	<800	<800	2935	4135	3793	3322	2935	1411	1411	3793	1613	10019	<800	8844	11201	3793	12068	11201	<800	5101	1256	<800	3793
intal and pre ited by dashe Hindi	SeqDerMap	5520	6382	512	449	11460	6972	1622	18795	3673	604	390	2931	4070	3563	3161	2953	1412	1420	3891	1664	10199	187	8860	11402	3813	12235	11190	183	5121	1262	150	3580
ne experime are separa {I	FngrPrnt	8874	<800	3742	8026	7546	11037	1707	13664	3299	2370	4672	11711	4672	1559	<800	24363	15632	2038	10423	2897	752	5654	4304	11037	<800	<800	<800	10093	24363	3933	1897	7546
between the fragments EcoR	SeqDerMap	9698	9	3758	7910	7475	11060	1717	13748	3257	2383	4643	11799	4750	1573	127	23801	15962	1928	10495	2861	748	5736	4315	10971	562	587	543	10168	24765	3930	1918	7425

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus clone CH230-165J24, *** SEQUENCING IN PROGRESS
                                                                                                                                                                    Direct Submission
Submitted (28-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02154, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                Submitted (31-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA 4 (bases 1 to 89672)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MAR-1999) Genome Therapeutics Corporation, 100 Beaver
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 19604 TTCCCAGACTTCTGAGGATTCAATTCAGAGAAAAGAGAATAAAGCTCTTCTAAATTATAA 19663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TITCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Street, Waltham, MA 02154, USA
On Mar 2, 1999 this sequence version replaced gi:3818353
Location/Qualifiers
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Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="CIT987SK-1137I1"
                                             Smith, D.R.
Sequencing of Human Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AATTTGGGTGGATTGGCAACAAACTTCCTG 130
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HTG; HTGS_PHASE1.
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60.0%;
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                                                                                                                                                                                                                                                                                              Direct Submission
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Direct Submission
                                                                                             Unpublished
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                                                                                                                                        Smith, D.R.
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SOURCE
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                         REFERENCE
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havek, P., Hawes, A., Henderson, N., Hernandez, J., Haradak, P., Hanes, S., Hladun, S.L., Hodgson, A., House, S.M., Hines, S., Hladun, S.L., Hodgson, A., Hoguses, M., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Howels, M., Howells, S., Hume, J. Glebird, D., Jackson, R., Jang, H., Member, J., Chila, M., Jang, H., Johnson, R., Liu, J., Lula, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewat, L., Loulseged, H., Lozado, R., Martinez, E., Mangum, A., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martinez, E., Moleod, M., Moneill, T., Menenen, E., Moleod, M., Moneill, T., Menenen, E., Morgan, M., Morris, S., Murphy, M., Nair, L., Nankervis, C., Neal, D., Okwuon, G., Derez, A., Perks, K., Parks, K., Pasternak, S., Paul, H., Perez, L., Perks, K., Pasternak, S., Scherer, S., Regigs, F., Rives, C., Rodkey, T., Rojas, A., Rose, R., Ruilz, S.J., Sanders, W., Savert, G., Sharkan, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sorelle, R., Sosa, J., Stenders, W., Saron, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Sorelle, R., Sosa, J., Steinle, M., Saker, J., Walker, B., Mang, J., Wang, S., Warren, J., Wooden, H., Worley, K., White, F., Williams, G., Wang, S., Warren, J., Warren, S., Wang, S., Warren, J., Warren, R., Weit, K., Wilse, F., Williams, G., Wang, S., Wa
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 52161 bases at least Q40 Consensus quality: 58316 bases at least Q30 Consensus quality: 58316 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1014: contig of 1014 bp in length
1114: gap of unknown length
2133: contig of 1019 bp in length
2233: gap of unknown length
3360: contig of 1127 bp in length
3460: gap of unknown length
5209: contig of 1749 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Center clone name: CH230-165J24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium.
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Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Li,J., Lichtargee,O., Lieu,C., Liu,W., Loulseged,H.,
Lozado,R.J., Lucier,A., Lucier,R., Luura,R., Ma,J.
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mai,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabat,K., Morgan,M., Morris,S.,
Moser,M., Naal,D., Newrson,J., Newrson,N., Nauyen,A., Nauyen,N.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Perez,L.,
Pickens,R., Pace,A., Payton,B., Perez,L.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Shen,H., Stone,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,B., Vinson,R., Wanilams,G., Walliamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Williams,G., Wulliamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 77751 bases at least Q40 Consensus quality: 77839 bases at least Q30 Consensus quality: 83524 bases at least Q20
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE JOURNAL

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Smith, D.R.
Direct Submission
Submitted (09-APR-2002) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
On Mar 27, 2002 this sequence version replaced gi:15021986.
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Submitted (09-DEC-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CBlo ISA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 23115 TICCCAGACTICTGAGGATTCAATICAGAAAAGAGAATAAAGCTCTTCTAAATTATAA 23056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATAC 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%; Score 32.4; DB 9; Length 216031; 60.0%; Pred. No. 22; Live 0; Mismatches 36; Indels 0;
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                      Sequencing vector: N/A Sequencing vector: N/A Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 990315
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                                                                                                                                                                                                                                                                                     The true right end of clone RP11-506P9 is 2000 in this sequence.
                                                                                                                           Center: Genome Therapeutics Corporation
                                                                                                                                                                                                                                                  IMPORTANT: This sequence is the entire insert of clone RP11-295023.
                                                                                                                                                                               Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                             Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .216031

/organism="Homo sapiens"

/db xref="taxon:9606"

/chromosome="10"

/clone="RPL1-295023"

/clone="RPC1-11"

66448 a 40595 c 41405 g 67583 t
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Caenorhabditis elegans
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Homo sapiens chromosome 10 clone RP11-295023, complete sequence.
AC011328
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Submitted (06-OCT-1999) Genome Therapeutics Corporation, 100 Beaver
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Submitted (28-MAR-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 44187 GTATATGTATGTATGAGTGCGCCGTGTACTTTCTTGACACACAGATGCCTCTGTACTGGAAC 44246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Therapeutics Corporation Sequencing Center: Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGGAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.4; DB 2; Length 127049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 36; Indels
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                                                                                        of 2425
                                                                                                           unknown
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Best Local Similarity
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AUTHORS
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JOURNAL
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VERSION
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join(10026. 10085,10140. 10243,10301. 10410,10454. 10577,
10631. 10699,10984. 11102,11150. 11298,11633. 11980)
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MEKIANNTCIRLIPRTNQPDYAEINNKKGGGCYASIGRFPGKNVVMLESNDDQSCIQE
DTVIHELFHVIGLWHEHRARDRDAFINNLYKNIEPAQYQFEKLSSRDTYSSVPUY
NSVMHYDENAFAKPGKISMYTKDSKPQKVJGHPKDASSNDYKKVCAIYHCSKCMHQDF
QQIVEQRIFLENNPITINAPVQQGDSCTDRLGICPMLKSREMLNCKVMATFCCSSCSA
PTSTTTTTSGTPSDGSLWQRIKSIFQ"
                                                                                             AAETICQQLRSSVIKNTSSIAPYDCGKVKWNYEDARAATLDDIGKSIHQQLVLFIEWA
KSELPGREFAAQAQQAALLKGGAASIIVLGVAYRSICLTVENTTCLANDTLLPKEHATQ
VGDINCVVCRIIDELVNPRRRINDDILEVALKALLEFNPVVREINQSPYRARXYE
LRSLQRRCTDKALENMEDESMDCRSGKLILLLIPSLQAIAQQLVEDVQLARLFGLVNVD
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*** SEQUENCING IN PROGRESS ***,
                                   /translation="MVEBICHICNDKSTGKHYGAISCDGCKGFFRRSIRKRYHYQCRF
EQNCDVTKNKRNACRACRLQKCVKAGMKSNAIQNERDAIGKRKKTTGAEKEDLIDQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDIKQLLLSIILTVSVVNGRGRRINIYGAENGKSDIVQLRGPAE
                                                                                                                                                                                                                        SSTGNFYFEKQNNERNILVIGNFQNLNPEPGEFYFKLFQMWNMHNKFCLVYLRRIGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(10026. .10085,10140. .10243,10301. .10410,10454. .1
10631. .10699,10984. .11102,11150. .11298,11633. .11980)
/gne="T23H4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Genefinder
contains similarity to Pfam domain: PF01400 (Astacin
(Peptidase family M12A)), Score=220.8, E-value=6.5e-63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4271 AAAAATGACGACTTCTAGCAACAATTTCATAATTCCAGGCAGCTCTTCTCAAAGGCGGTG 4212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 154139)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTG 110
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                                                                                                                                                                                                                                                                                                                                                                         /product="tRNA-Glu"
/note="TTC Glu E-tRNA
predicted using tRNAscan-SE-1.11
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Rattus norvegicus clone CH230-9F24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 32.2; E 51.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="SPTREMBL:P91828"
            xref="SPTREMBL:P91829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB05814.2"
/db_xref="GI:7160734"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary prediction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to tRNA-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2124 g
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/gene="T23H4.t1"
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/gene="T23H4.t1"
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HTG; HTGS PHASE1.
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AC095797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1039,1078. .1163,1269. .1519, .2161,2208. .2331,2377. .2469,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(354. .430,794. .908,952. .1039,1078. .1163,1269. .1519,
1568. .1664,1728. .1934,1985. .2161,2208. .2331,2377. .2469,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(3392. .3563,3605. .3654,3700. .3805,
3853. .4032,4088. .4233,4428. .4583,4800. .4942,4992. .5057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVTAFEDDNLPEVVNREYTWVSYYQWVPFFLVYVAFSFYAPCLIWRLFYDKSGIRLKD
IMGFANDKANVVPTORTANIRGLSAHLSSPFKRIRFRIGEKPFYHKVFRFFFIRWRYYES
YLTYLYLAIKCLFLWANVLTOWYFMSFPLELDSHRYYGYGIFYDLIMGKGWKESSNFPV
VTYCDMOIRILGHVQRHTVQCVLVINIFTEKIFFILMLWYTMISLISFGSILSWIFAS
IPFUGRAFFTARLELADVPFKSFRFKQELDEFVRDYIKIDGIFVLRMITHGGILMC
TDIYDWMDQFLQESGHATIRFILEDKSYGDDYDRSASAGGLSIEPSLRKTSVLVPL
MSREDHHLDQSPFTAPAQFLRPSSRNASAANV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Similarity to Mouse hepatocyte nuclear factor 4 (SW:R49698), contains similarity to Pfam domain: PF00104 (Ligand-binding domain of nuclear hormone receptor), Score=153.8, E-value=9.76-43, N=1; PF00105 (Zinc finger, C4 type (two domains)), Score=149.3, E-value=4.1e-44, N=1"
                                                                                                                                                                                                                                                                                                                                         neighbouring submissions.
The true left end of clone T2344 is at 1 in this sequence. The true right end of clone T2344 is at 23430 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone F52F12 is at 12215 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence 283235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MDAQALPQHSASSNKTGGSPGARVPRMVFAEIVGTLSFLQPQAD
DDIFDRLHYYYTTTFLLLTAVLISLKMFGGRPIECWLPAEYKSSWEDYTEMYCWARNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The end of this sequence (12215. .12318) overlaps with the start of
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT This sequence is not the entire insert of clone T23H4. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (3392. .3563,3605. .3654,3700. .3805,
3853. .4032,4088. .4233,4428. .4583,4800. .4942,4992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder
contains similarity to Pfam domain: PF00876 (Innexin)
Score=391.2, E-value=3.2e-114, N=1"

    12318
/organism="Caenorhabditis elegans"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(354. .430,794. .908,952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /proteIn_id="CAB05813.2"
|db_xref="G1:7160733"
|db_xref="SPTREMBL:P91827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /proteIn_id="CAB05815.1"
/db_xref="G1:3880160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:6239"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2809. .2945)
/gene="T23H4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="T23H4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5163. .5319))
/gene="T23H4.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence Z83228.
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consists of 73 contigs. The true order of the pieces

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Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbard, Benton, J., Binage, K., Blankenburg, K., Bomnin, D., Bouck, J., Bowle, S., Briewa, M., Brown, B., Brown, M., Bryant, N. P., Bouck, J., Barbard, B. Brown, B., Brown, B., Brown, M., Bryant, N. P., Bouck, J., Charko, J., Davila, R., Davy, Carroll, L., Dathorne, S. R., David, R., Davila, M., Douthwaite, K. J., Denger, H., Dugan, Rochas, S. R., David, R., J., Barnhaite, K. J., Earnhaite, C., Edhaj, C., Edhaj, C., Escotto, M., Fallis, T., Garga, D., Carner, T., Barnhaite, K. J., Harrandez, G., Harris, K., Hart, M. Havlah, P., Harsandez, J., Harrandez, G., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Harr, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kallson, E., Kallson, E., Kallson, E., Kallson, E., Karlsson, E., Kallson, E., Karlsson, E., Kallson, E., Licherage, O., Lisau, C., Liu, J., Liu, W., Loulseged, H., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martin, R., Markon, J., Nowtson, J., Nowtson, J., Nowtson, J., Nowtson, J., Nowtson, J., Nowtson, J., Rives, M., Rois, R., Mawhiney, E., Polchell, T., Mobabat, K., Morgan, M., Rois, S., Scott, G., Shen, H., Shooshtari, N., Savery, G., Sherer, S., Sott, M., Spark, R., Shankon, J., Martin, R., Waode, R., Norden, S., Scott, G., Shen, H., Shooshtari, N., Savery, G., Wang, G., Williamson, A., Willersk, R., Sonnik, S., Warren, R., Wand, M., C., Wu, Y., Wu, Y. F., Ray, M., Charle, R., Shankon, J., Raherisa, R., Shankon, J., Raherisa, R., Shankon, J., Saveri, R., Wand, W.C., Wu, Y., Wu, Y. F., Ray, M., Martin, R., Wooden, S., Warren, R., Walliamson, A., Willalla, S., Waller, S., Waller, S., Wa
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Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:20975907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 84102 bases at least Q40
Consensus quality: 96883 bases at least Q30
Consensus quality: 96268 bases at least Q30
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------- Project Information
Center project name: GDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: CH230-9F24
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Direct Submission
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\* NOTE: Estimated insert size may differ from sequence length \* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft\_data.html). \* NOTE: This is a 'working draft' sequence. It  $\operatorname{currentl}_{\overline{Y}}$ 

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
not known and their order in this sequence record is
                                                                                                                                                         1319: contig of 1319 bp in length
1419: gap of unknown length
3097: contig of 1519 bp in length
4547: contig of 1450 bp in length
4647: gap of unknown length
5928: contig of 1181 bp in length
5928: contig of 1181 bp in length
7278: contig of 1350 bp in length
7378: contig of 1350 bp in length
8705: contig of 1357 bp in length
8705: gap of unknown length
8705: gap of unknown length
10379: contig of 1574 bp in length
10379: contig of 1574 bp in length
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gap of unknown l
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oks, S.L., Amaratunge, M.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Buok, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Bunk, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carcon, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M.L., Davis, C., Day, Carroll, L., Dederich, D.A., David, M.L., Davis, C., Day, Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Gariel, J.H., Gevola, M., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Holloway, C., Hollins, B.,
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Rattus norvegicus clone CH230-297018, *** SEQUENCING IN PROGRESS
***, 27 unordered pieces.
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 15, 675 genomic DNA of 21q21.1-q21.2 Published Only in DataBase (1999)

2 (Dases 1 to 151675)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
Submitted (13-SEP-1999) Masahira Hattori, The Institute of Physical
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                                                                                                                                                                                           and Chemical Research (RIXEN), Genomic Sciences Center (GSC); Kitasato Univ. 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Uapan (E-mail:hattori@ges.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Pax:81-42-778-9924) On Nov 9, 1999 this sequence version replaced gi:5881381. Sequence updated (08-Nov-1999).
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/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="21"
/map="21q21.1-q21.2"
/clone="B15H23"
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1 (bases 1 to 151675)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lorado, R., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lozado, R.J., Li, L., Lichterge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLecod, M. P., Meador, M., Meirker, M., Neal, D., Newtson, M., Nguyen, A., Morris, S., Mickens, E., McLecod, M. P., Newtson, M., Nguyen, A., Nguyen, N., Notekens, E., Werken, S., Oguh, M., Okwonu, G., Peters, L., Pickens, R., Purlis, P., Perey, J., Perez, L., Peters, L., Pollack, M., Ren, Y., Rives, M., Rojas, A., Pannus, E., Pu, L.L., Quiles, M., Stone, H., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Ward, Wang, G., Walliamson, A., Waren, R., Wand, S., Warren, R., Warhington, C., Walliams, G., Walliams, G., Warren, R., Washington, C., Wallington, S., Weinstock, G. and Gibbs, R., Marchilla, S., Nelson, D., Weinstock, G. and Gibbs, R., Dubblished
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* NoTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 27 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 13432 bases at least Q40
Consensus quality: 137161 bases at least Q20
Consensus quality: 139528 bases at least Q20
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gap of unknown length
contig of 1151 bp in length
app of unknown length
contig of 1498 bp in length
gap of unknown length
contig of 1220 bp in length
contig of 1220 bp in length
contig of 1820 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-297018
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Direct Submission
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500 TACAGGAGTGCTGACACACACCCAACAGGGAGGTCAAGCCACTGTCAGAGACAGCAAGT 559
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/db_xref="taxon:10116"
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1. (Dages 1 to 169329)
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27. Habrooks 5.L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Edimage, K.C., Blankenburg, K., Bonnin, D., Bouck, J., Barbaria, J., Benton, J., Edimage, K.C., Blankenburg, K., Bonnin, D., Bouck, J., Carter, M., Bryant, N.F., Carter, M., Bryant, N.F., Carren, G., Chen, R., David, R., David, R., Davis, C., Davy-Carroll, L., Dager, V., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Carraguto, D., Fland, R., Durbin, K.J., Harris, K., Harris, G., Harris, K., Harris, M., Havlak, P., Haues, S., Haniton, K., Harris, C., Harris, K., Huber, J., Jolivet, S., Hume, J., Jackson, L.E., Jacobson, B., Jai, Y., Johnson, R., Jolivet, S., Joddah, S., Karlsson, E., Kalls, Y., Anderson, M., Holloway, C., Hollins, B., Harris, K., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Licharge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Marlak, P., Hales, B., Marliner, E., Marlinery, E., Martin, R., Martin, C., Mulles, M., Nokeson, E., Radin, M., Nokeson, J., Newtson, J., Socht, G., Shen, H., Shoshtari, N., Satek, A., Tador, Y., Willald, M., Svatek, A., Tador, Y., Willald, M., Svatek, A., Tador, Y., Willald, M., Svatek, A., Rador, M., Rojas, A., Rooshtaris, A., Tador, C., Taylor, T., Tador, S., Warren, R., Wang, G., Willa, M., Y., Wu, Y., Wu, Y., Wu, 
                                  AC118484 165929 bp DNA linear HTG 18-JUL-2002 Rattus norvegicus clone CH230-312N5, *** SEQUENCING IN PROGRESS AC118484 AC118484. GI:21745726
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                                                                                                                                                                                                                                                                    Norway rat.
Rattus novregicus
Bukaryota, Antazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pizeces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                            Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 122701 bases at least Q40
Consensus quality: 128016 bases at least Q30
Consensus quality: 131913 bases at least Q20
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                  Center project Information
Center project name: GTTM
Center clone name: CH230-312N5
Contact: hgsc-help@bcm.tmc.edu
                                                                                     ----- Summary Statistics
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* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishli, K., Totoki, Y., Choi, D. K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Totoki, Y., Choi, D. K., Soeda, E., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Samermann, W., Rosenthal, A., Kudo, J., Shibuya, K., Mawasaki, K., Asakawa, S., Shintani, A., Saski, K., Magamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Blocker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori, M., Pujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Toroki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Toroki, Y., Choi, D.K., Soeda, E., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Astakawa, S., Shintani, A., Saski, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, M., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Hennischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
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Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717287.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * Keio University School of Medicine, Molecular Biology, * Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail: info.genome@gbf.de * URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute of Molecular Biotechnology, Genome Analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * Max-Planck Institute for Molecular Genetics,

* Ihnestrasse 73, D-14195 Berlin, Germany,

* e.mail: info-chrzl@molgen.mpg.de

* ME: http://chrzl.rz-berlin.mpg.de/

AL163234: Submitted (10-Apr-2000).
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* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The DNA sequence of human chromosome 21
Nature 405 (6784), 311-319 (2000)
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• e.mail: nshimizu@dmb-med.keio.ac.jp

• URL: http://www.dmb.med.keio.ac.jp/
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176350 bp DNA linear HTG 19-JUN-2002
Papio cynocephalus anubis clone RP41-474E21, WORKING DRAFT
SEQUENCE, 1 ordered piece.
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HTG; HTGS PHASE2; HTGS_DRAFT.
olive babbon.
Papio cynocephalus anubis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 243472 CAACAAAAAGATAACTCACTGAAGCTTCAGATAACCATTAGCATGTTTTAGCAATAAATT 243531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 243532 ATTTTTAACGAACATGTCTACATTTTTAGAGATCATGCTATTATACACTTAATAGGCTAC 243591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 TCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTTGGCAACAAACT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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AC092513
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KEYWORDS
SOURCE
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Cercoptthecines, Papio.

E (bases 1 to 176350)

Akhter, M. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,
Mcloskey, J.C., McDowell, J., Pagnirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Netherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.,
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 176350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (19-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 19, 2002 this sequence version replaced gi:14717326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: aml
Center clone name: 474E21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Center
                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 176350)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                       Green, E.D.
                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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DEFINITION
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                                                                                                                                     KEYWORDS
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* Infalse: contig of 176150 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 135000; agarose-fp
Insert size: 172000; pulse-field-gel
Insert size: 176350; sum-of-contigs
Quality coverage: 17.59x in Q20 bases; agarose-fp
Quality coverage: 13.81x in Q20 bases; pun-of-contigs
Quality coverage: 13.47x in Q20 bases; sum-of-contigs
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source

FEATURES

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RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Brewn, M., Brown, B., Bryant, N.D., Buhay, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavacz, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delagac, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delagac, O., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Footd, J., Rostet, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Halle, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Halle, S., Hames, J., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, M., Liucier, R., Liu, M., Loulseged, H., Lozado, R.J., Lux, Lucier, R., Luna, R., Martinala, C., Liu, J., Liu, M., Lucier, R., Massey, E., Mawhiney, E., Matchin, R., Martindale, A., Martinez, B., Martings, C., Mitchell, T., Mohabbat, K., Morgan, M., Morsis, S., Moser, M., Neal, D., Newtson, J., Newtson, J., Nguyen, N., Nguyen, M., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC094911 185829 bp DNA linear HTG 10-JUL-2002
Rattus norvegicus clone CH230-616, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 108096 ATTCAAATAGTTATTCAATTGATAAAATAAGCAATATTAGATACAAGTAAACAATATTAG 108155
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone overlaps with GenBank Accession Number AC092407 clone RP41-402M16 (center project name amk)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ture 136968. 176350
/note="clone overlaps with GenBank Accession Number
AC022515 clone PR91-6601 (center project name ami)"
54537 a 33462 c 34511 g 53840 t
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'organism="Papio cynocephalus anubis"
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54.8%; Pred. No. 34;
Live 0; Mismatches
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/note="assembly_fragment
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1. .44288
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Birect Submission

As Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sa (bases 1 to 185829)

Sa Worley, K.C.

Direct Submission

Al Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 9, 2002 this sequence version replaced gi:17941708.
               Oragunye, N. Oviedo, R., Pacce, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Riveer, R., Rojubokan, I., Rolfe, M. Raiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutten, A., Svatek, A., Tabor, P., Tamerisa, R., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williams, G., Williams, G., Williams, G., Walliams, G., Wal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 129812 bases at least Q40 Consensus quality: 134491 bases at least Q20
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f unknown length
g of 1096 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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gap of unknown 1
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Center clone name: CH230-616
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COMMENT

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RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bonton, J. Biaeva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chavez, D., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhajo, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Fortd, J., Garza, N., Gall, R., Harls, C., Escotto, M., Harris, C., Harris, K., Hart, W., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, W., Havlak, P., Hawes, A., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jackson, B., Jia, Y., Johnson, R., Jollovet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, B., Jia, Y., Lucier, M., Liu, J., Liu, W., Lucier, R., Liu, J., Liu, J., Li, Z., Lucier, A., Lucier, R., Luna, R., Martina, R.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 97037 CAPATITCAGGACACAATAAATIGGITITAAGAGGCAAGTICAIAGCACTAAGGACACAATA 97096
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unknown length
of 2251 bp in length
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gap of unknown length
contig of 2979 bp in length
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Best Local Similarity
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Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Soonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, N., Tamerisa, N., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Warde, W., Willalan, D., Vinson, R., Wang, O., Williams, G., Wallington, R., Washington, C., Wallington, S., Walstscok, G. and Gibbs, R., Walliams, G., Wallington, S., Weistscok, G. and Gibbs, R., Sorrilla, S., Nelson, D., Direct Submission Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 188412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2002_this sequence version replaced g1:20514550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h * NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs the true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid,
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 128358 bases at least Q40
Consensus quality: 137074 bases at least Q20
Consensus quality: 144224 bases at least Q20
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1310: gap of unknown length
2878: contig of 1468 bp in length
4331: contig of 1468 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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AC084753 193858 bp DNA linear HTG 15-WAY-2002 Mus musculus clone RP23-111E15 strain C57BL6/J, WORKING DRAFT SECURICE, 14 unordered pieces.
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2 (bases 1 to 193958)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 193958)
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Chemistry: Dye-terminator Big Dye; 100%
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 188704 at least Q30
*Consensus quality: 183136 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 193698 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 6.5 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGA 158
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g of 5156 bp in length
f unknown length
g of 7968 bp in length
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                                                                                          g of 5523 bp in length
f unknown length
g of 3941 bp in length
f unknown length
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unknown
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arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                          entig of 35267 bp in length gap of unknown length contig of 2721 bp in length contig of 2721 bp in length contig of 30274 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 14861 bp in length gap of unknown length gap of unknown length
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185183. .188376
/note="assembly_name:Contig17"
188397. .191981
/note="assembly_name:Contig16"
192002. .193958
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55909 a 39869 c 41311 g 56548 t
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| Moote = "assembly_name:Contig24"

127524. .141784

| Moote = "assembly_name:Contig23"
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[52095. .162822
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[62843. .173906
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173927. .181599
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181620. .185162
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/clone="RP23-111E15"
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ORIGIN
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 17-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL512599 157750 bp DNA linear PRI 17-AUG-2003
Human DNA sequence from clone RP11-115D7 on chromosome 1, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group, Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-115D7 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirites: thunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 19, 2002 this sequence version replaced gi:22204192.
                                                                                                                                                                                      39450 CCAAGAGAATAAAACAAAACTAAAACAACAGAACTAATGTTGGATGAATGCCATCATGC 39391
                                                                                                                        65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                                 0; Gaps
   DB 2; Length 193958;
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VECTOR: pBACe3.6.
                                                              0; Mismatches
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32684 c 33292 g 46053 t
15.4%; Score 31.8; I
57.6%; Pred. No. 35;
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/chromosome="1"
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AL512599.33 GI:22316102
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                                                              57; Conservative
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                                Local Similarity
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Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Canazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., FitzHudh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, E., M., Kells, C., LaRocque, K., Lamazares, R.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Kalls, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
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Mus musculus clone RP23-119G12, WORKING DRAFT SEQUENCE, 23 ordered
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-119G12
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                                                                                                                                                                                           Db 104456 TGGTCAATTTGATTTTTCACATGGTTTAAAAGACAGGGTTGCCAGATAAAATACAG 104515
                                                                                                                                                                                                                                                                                                                    94 GCGATACAATTTGGGTGGATTGGCAACAACAACTTCCTGTGACTAACAGGTCCATAGTTTTT 153
                                                                      Gaps
                                                                                                                               34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAAC 93
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   DB 9; Length 157750;
                                                                   64; Indels
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
Score 31.6; DB
Pred. No. 40;
0; Mismatches
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52.2%;
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                                                                   70; Conservative
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McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olliver, J., Peterson, K., Phukhang, P., Paterre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., V. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25.4PR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 25, 2002 this sequence version replaced gi:18450059. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
Contact sequence tame: L10730
Center project Information
Center project name: L10730
Center clone name: 119 G 12
Center clone name: 119 G 12
Sequencing vector: Plasmid; not, 100% of reads
Sequencing vector: Plasmid; not, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 198517 bases at least Q30
Consensus quality: 201511 bases at least Q30
Consensus quality: 202745 bases at least Q20
Insert size: 207000; agarose-fp
Insert size: 203415; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; sum-of-contigs
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1 85: contig of 85 bp in length
86 185: gap of 100 bp
186 32349: contig of 32164 bp in length
32350 32449: gap of 100 bp
32450 33486: contig of 1037 bp in length
33487 33586: gap of 100 bp
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33587 35126: contig of 1540 bp in length
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46918: contig of 2039 bp in length
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116156 116255: gap of 100 bp 116256 134632: contig of 18377 bp in length 134733 158355: contig of 23623 bp in length 158356 186455: gap of 100 bp 158456 186958: contig of 22403 bp in length 16859 186958: gap of 100 bp 186959 186959: contig of 24540 bp in length 186959 205498: contig of 24540 bp in length
                                                                                  82475 82574: gap of 100 bp
82575 97310: contig of 14736 bp in length
97311 97410: gap of 100 bp
                                                                                                                       oof 100 bp contig of 18745 bp in length
                66001: gap of 100 bp
72672: contig of 6671 bp in length
                                             72772: gap of 100 bp
82474: contig of 9702 bp in length
65901: contig of 4382 bp in length
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205599 205615: contig of 17 bp in length.
Location/Qualifiers
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/clone="RP23-119G12"
/clone_lib="RPCI-23 Female Mouse BAC"
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3587. .35126
note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
|58456. .180858
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205599. .205615
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10197. .42396
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note="assembly_fragment"
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16256. .134632
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80959. .205498
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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186. .32349
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MSQLDLTSASHLGTSTSKKKSGWVSYKDDGILSFIWQKRYLMLHDSYVALYKNDKQND
DAILKIPLTSIISVSRTQLKQYCFELVRCSDRNSVSSGSSSSLNVSSDSNSKKSIYIA
                                                                                                                                                                                                                                                                                                                                                                                                          PLN 11-AUG-1997
                                                                                                                                                                40444 TATTATAAAGCTAGCTATATTTCAGAGCAACTGTACAGGCAGACCAAGAAGTCATTTTTC 40503
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Submitted (29-APR-1996) Data collected by MIPS on behalf of the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152
                                                                                                                                                                                                      82 GAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGG 141
                                                                                          0; Gaps
                                                                                                                             22 TATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATA 81
                                                        Length 205615;
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S.cerevisiae chromosome XIV reading frame ORF YNL298w.
Z71574 Y13139
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                                                                                        79; Indels
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Location/Qualifiers
1. .3277
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Maurer, C.T.C., Urbanus, J.H.M. and Planta, R.J.
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/db_xref="taxon:4932"
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                                                        DB 2;
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/db_xref="SWISS-PROT:P48562"
                                                    15.3%; Score 31.6; DB 50.0%; Pred. No. 40; tive 0; Mismatches
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clone_end:T7
vector_side:right"
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/gene="CLA4"
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                                                    Query Match
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Matches 79; Conservative
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                      44; Conservative
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    Best Local Similarity
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QGPSPSPSPSPSPSPLHNWTNPYSKOPOSPLSSOSTONOAL PRYAQNSSPTAAH
PQPQRTAPKPPISAPRAPYPSNONATSNTHVQPVAPKNDQSTPQTMRQAPKRPDADVA
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FLEAYLRTDDDLMVVMEFMEGGSLTDIIENSPTNDNSHSPLTEPQIAYIVRETCÇGLK
FLHDKHIIHRDIKSDNVLLDTRARVKITDFGFCARLTDKRSKRATMVGTPYWMAPEVV
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Cvrckova, F., De Virgilio, C., Manser, E., Pringle, J.R. and Nasmyth, K. Ste20-like protein kinases are required for normal localization of cell growth and for cytokinesis in budding yeast Genes Dev. 9 (15), 1817-1830 (1995)
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Submitted (03-NOV-1994) F. Cvrckova, IMP, Dr Bohr-Gasse 7, 1030
Wien, AUSTRIA
                                                                                                            1884 AACAGCTCCAAAAGCCACCACTATCAGCTCCAAGGGGGGCGCTACCCATCAAATCAAATGC 1943
                                                                                 136 AACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGT 195
                                             Gaps
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    15.2%; Score 31.4; DB 8; Length 3277; 67.7%; Pred. No. 39;
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                                           Indels
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    /organism="Saccharomyces cerevisiae"

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589. 5117
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/evidence=experimental
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/gene="CLA4"
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15.2%; Score 31.4; DB 8; Length 3858;

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Query Match

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GASTVTLAXPKDTVLSALLITTIVVVGYSLTALSERFENVLNSATSIYYWLNGLWIMI

GMGLTALLFGNNTHSSKFNLLYGWLGAILFTAYLFIDTQLIFRKVYPDEEVRCAMMLY

LDIVNLPLSILRILASSNDDN"
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TNISYPSSSDSVLTKSNGSSEVYKRKEEVVKXILHGKFTKNNTHLTFSSVVEDKNFHK
NNKSLTYNDTMLYYLNLPQKVKISLSTGCLGFRKAARGEYEAAPQTSGRMFELIKEKNM
LNKDIEVNMDDFGKRAAFISALLGASVVKKVVKISDATKLKFGGVRSPKMRRL"
complement (1376. .2269)
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales;
Saccharomycetales;
Saccharomycetaces; Saccharomyces.

(bases 1 to 3003)

Maurer, K. C., Urbanus, J. H. and Planta, R. J.
Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putcative serine-(threonine protein kinase gene
                                                                                                                                  1953 AACAGCTCCAAAGCCACCAATATCAGCTCCAAGGGCGCCATACCCATCAAATCAAAATGC 2012
                                                                   136 AACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGT 195
   Gaps
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21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharomyces cerevisiae"
/strain="FY1679"
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="YNL0397"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                       30003 pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Yn10405p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="YNL0397"
633. .1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQPQRTAPKPPISAPRAPYPSNQNATSNTHVQPVAPKNDQSTPQTMRQAPKRPDADVA
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RIVQEDLFINDTEDLPVEEIYKLDEPAKKKQKAKKDKREGEIKKSAIPSPPPEGGVSR
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FLHDKHIIHRDIKSDNVLLDTRARVKITDFGFCARLTDKRSKRATMVGTPYWMAPEVV
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                                                                                                                 ISDGYASYIPKSCWRTLEPSRSKFSLAIQDPGDPNNNISRGSFNMKDIKKAFAGAFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQNVPNQQYPKMRNGHSPTNGQFPRĞPMHPNNSQRSLQQQQQQQQQQQQQQQQPPHH
QGPSPSPSPSPSPLPYRPHHNMINPYSKQPQSPLSSQSTQNQAIPRYAQNSSPTAAH
IRNHCHSKORRIADWLTSEIKDFVHYISPSKNEIKCRNRTIDKLRRAVKELWSDADLH
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                                                                                                                                                                                                                SKLKRKVKKTDQGSLLHQNNLSIDDLMGLSENDQESDQDQKGRDTLRDKMRNHHWKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRFLSVCLCVDVRYRASTEELLHHGFFNMACDPKDLTSLLEWKE"
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                            gene
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DLLKARFFLVGNKIDLYKERQVTHYDVVQMVQEMQLKHGIKISGNFEVSCKWVNVVER
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ALRFTAGARAKIVKAGGECITLDQLAVRAPKGQNTLILRGPRNSREAVRHFGMGPHKG
KAFRILSTGRKFERARGRRRSKGFKV"
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                                                                                                                                                                                                                                                                     ILSYCRELLTRAEMSRSARLRHQQQQQHKDLGLKKTVVNHRLSMKEKRKRYSSNDFEK
EFKDINHFADETSDFGNPNIGDDNNHEMADPNEIVIETRSTIGIDIKTNLVNIDNRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join (4435. .4849, 5401. .5420))
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                                                                                                                                                                                                                                                                                                                                                                                                                       NTVDITKPNDDIANNQSICCV"
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                                                           960. .4027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="YNL0415"
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                                                                                                                       codon start=1
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ASATLQQLIDEĪFDRLŠIESVVDDKQYEVLISNSESIKVNVYRYDANKLFDNICSLNE
ISSNGAVSDEEMLLDIGDIPIDYGLEILESILKNSQKNLLECQDLQYLLRVKAIPLLL
                                                                                                                                                                                                                                                   RCISSSRHFSTAVRSCRCLKLLIRKEYLSILELELEVILSLLIHGISVESNLSGWQRV
LSLELFKDLSQDPEIVNTLYMDYDNYPDKKHVFKYLLKECIVLLNSPEYITFLAPSKV
VEKMDSPLITTENSTVKTKFMHLLDKSNAPSINITYIISLILTICNHLCEGLNKSALB
                                                                                                                                                                                                                                                                                                                                                                                                          SSPLEKKI EDKEREEGTGNDSTVVKVYSGLFSGLFELNKLFLYSTSLETS I FHLVVRA
SQLAHSANVLSLKDKLRACKKLFSILITINNVTSRSNOYSFRDYSKSAKOHTRNISTS
SVTTSPVESTKNESRS SLADSAQUKEMKRRIHPRNISSRQVSLLRALISLSISLGPIFD
SESWRYTFLIWQWITYYIYGPSADFKESFYSEDIPPPPILIKSDVTSIESSLTKFFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSSYSCSTFHLVLTRLILDSKNTLTLEQTNLNLNNDIGYHPLDAKDEIIPCIYNKAFF
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KKATNEVGNSDEQDNKVKQFGTLENLVIDSLMATINSIKQLDIGKQEIYNGTINVESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILFQLLLTLKEILNEFGELLANSWTNIFNIINSPFEWTVEDTDFSVNEDIDDSSLFEG
IVQKHKNMIQVSYDVFKLISDDFLQSLPMSVIKFVIDTLVNFVSQKRNLNISFSSISQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTNDSKDTEILILLQLSTISILAFDTREKITKKLGPKLPKASLNRLPTFEAISYMSCS
NLRNRIAKIDQFGISTLKAKHILRILKNLAEIIKRKSLITGSESDEIPIWVLASNCFC
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                                           KRVHSFEELERHPDFALPFVLACQSRNÄKMTTLAMQCLQGLSTVPSTPRSRLSETLDA
FIBATHLAMEIQLKVLQVVPIFFKTYGKFIYGPLCKKLLLCCSNLLHVPNKAPVVVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKNLINCTNDDRVEVKNGAVQTFFRIIDSHSVCFPPWDLIFLEVIEPLLTKEWSTEEL
ENETDFINVTLQGLIKLYPEHFKDFKNNTTCAKEWSMLLDFLKRLLSSTSNNTKNAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLYQLISKYDAMTDEFVEKVLLLFNSAIKYPLLPEFVQDKTKPSSMQKAILSGLDIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCI FGSTTNPRFQTKYKCSLECLQDLVNFMLNTNEKLRKLTAPYLSAR I ALALRRY I S
DEYL I GRAP I PKLRKTELATLLNGLCVI LRGVLDQNSTLGNKQ I GVENLQTLSPLILR
translation="MAMNTGGFDSMQRQLEAELRSLSSESKRRNSTIRHASDKSIEIL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNYQTLLKEIITIEDVPSDILKKCCEIFTDYNITYSDLSTNASSKTEYDCIYELITGF
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100 bp
of 699 bp in length
100 bp
of 678 bp in length
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                   100 bp
of 693 bp in length
                                                                      100 bp
f 688 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 100 bp contig of 712 bp in length of 100 bp contig of 677 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases I to 64656)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-78J18
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                              12755 AACAGCTCCAAAGCCACCACATATCAGCTCCAAGGGCGCCATACCATCAAATCAAATGC 12814
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
136 AACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGT 195
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Mus musculus clone RP23-78J18, LOW-PASS SEQUENCE SAMPLING.
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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-------- Project Information
Center project name: L17941
Center clone name: 78_J 18
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Web site: http://www-seq.wi.mit.edu
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HTG; HTGS PHASE0.
Mus musculus.
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/note="Tigger3b repeat: matches 979. .1241 of consensus"
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8830 GGTCTTTAAGAAGGACATACATAACTCCCTTAAGAAACAGGAAAATACAGGTAAACAAGT 8889
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19: gap of 100 bp
30926: contig of 707 bp in length
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Further information can be found at the confirmation of the prince of the pr
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Human DNA sequence from clone RP1-23E21 on chromosome 6 Contains a
pseudogene similar to JAB1, an STS and GSSs, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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49. .151 of consensus"
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                                                                                                                                   'note="160 copies 2 mer aa 59% conserved"
                                                                                                                                                     8890 AGAAGCCCTTAAAGTGGAAACACAAAAATCCCTTAAAGAATCACA 8934
95 CGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACA 139
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http://www.chori.org/bacpac/home.htm
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/clone_lib="RPCI-1"
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/note="Mill repeat: matches 304, .367 of consensus"
1418. 14525
/note="Mill repeat: matches 46, .257 of consensus"
15291. 15512.
/note="111 copies 2 mer as 56% conserved"
15631. 16691
/note="Mill repeat: matches 1. .1071 of consensus"
17046. .17494
/note="Mill repeat: matches 3108. .3556 of consensus"
complement(17483. .18190)
/note="match" GSS: Em:AQ528649"
/note="match" GSS: Em:AQ528649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSg/x repeat: matches 135. .295 of consensus"
0448. .30471
         note="Tigger3b repeat: matches 1. .849 of consensus"
193. .3335
                                                                                                                                                                                                                     0027. .10219
note="LTR16A repeat: matches 217. .436 of consensus'
                                         note="MLT11 repeat: matches 230. .354 of consensus"
862. .5939
                                                                                                                                                                                                                                                                                                                                  note="AluSc repeat: matches 244. .299 of consensus"
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Anote="MIR repeat: matches 54. .190 of consensus"
20856. .20994

Anote="MIR repeat: matches 29. .175 of consensus"
21044. .21135

Anote="MILTIA2" repeat: matches 7. .369 of consensus"
21383. .23734

Anote="MILTIA2" repeat: matches 7. .369 of consensus"
27384. .27554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"MIR repeat: matches 183. .205 of consensus" 0472. .30509 inote-"L2 repeat: matches 2648. .2685 of consensus"
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33019. .33473
.hott="match: GSS: Em:AQ593411"
complement(33062. .33656)
                                                                                                      note="1.2 repeat: matches 2628. .2710 of consensus"
note="1.2 repeat: matches 100. .204 of consensus"
note="1.5 copies 4 mer tgtg 98% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30510. .30524
/note="MIR repeat: matches 205. .261 of consensus"
complement(32107. .33024)
                                                                                                                                                                                                                                                               1084. .11366
note="AluY repeat: matches 12. .293 of consensus"
1403. .11511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 1. .230 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                            note="AluY repeat: matches 1. .249 of consensus" 2009. .12075
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7620. 17647
note="14 copies 2 mer ac 92% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (32107. .33024)
note="match: GSS: Em:AQ743106"
complement (32486. .33025)
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note="match: GSS: Em:AQ182012"
complement (17919. .18184)
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32593. .32717
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8089. .18447
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note="match: GSS: Em:B41655"
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/note="MER30 re
18750. .18924
/note="MER34 re
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note="L2 repeat: matches 1997. .2445 of consensus"
4142. .44368
note="MLT1A1 repeat: matches 138. .365 of consensus"
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/note="Aluo repeat: matches 1. .296 of consensus" 50252. .50968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 2648. .2700 of consensus"
3605. .44064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4373. .44570
note="L2 repeat: matches 1747. .1966 of consensus"
                                                                                                                                                                                                                                                                                                              /evidence=not_experimental 35714. 36025
/note="AluSx repeat: matches 1. 312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluSx repeat: matches 1. .297 of consensus"
3460. .43470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .80 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45847. .46142
/note="AluY repeat: matches 1. .296 of consensus"
complement(46105. .46452)
/note="match: GSS: Em:AQ817722"
46261. .46313
/note="MADB1 repeat: matches 28. .80 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="FRAM repeat: matches 0. .152 of consensus"
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Best Local Similarity 57.7%; Pred. No. 45;
Matches 56; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                             17734. 37761
'note="14 copies 2 mer ac 100% conserved"
18271. 38566
                                                             /note="60 copies 2 mer aa 61% conserved"
complement(33264, .33659)
/hote="match: GSS: Em:AQ090546"
33775, .33800
                                                                                                                              /note="dJ23E21.1" (similar to JAB1)
match: proteins: Tr:015386 Tr:035864"
/pseudo
/note="match: GSS: Em:AQ419443"
33104. 33519
/note="match: GSS: Em:AQ090303"
33130. 33249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match: STS: Em:G61943
latch: GSS: Em:AQ285562"
9795. .49939
                                                                                                                                                                                                                                                                                                    'codon start=1
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27 GAGTICTTGGTCAATTTCCAGGACACAGATGGTTCGGTCCAAGAACAGGATAATAGAACT 86 ઠે

87 AAGCAACGCGATACAATTTGGGTGGTTGGCAACAAA 123

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## Db 42250 TGCCAAATTGTGAAGCTGGATGAAATTAGGCATCAAA 42286

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Elirran, N. Bastien, V., Buobaum, C., Lander, E., Allen, N., Anderson, S., Barran, N. Bastien, V., Bougialavity, L., Boukhgalter, E., Brown, A., Camarata, J., Camopojano, A., Chang, J., Choppel, Y., Colangelo, M., Conlins, S., Collymore, A., Coch, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitthugh, M., Gage, D., Galagan, J., Cardyna, S., Cinde, S., Goyette, M., Candmill, M., Marquis, N., Marquis, N., Marthews, C., McCatthy, M., Marquis, N., Marquis, N.
                                         ACO91647 173368 bp DNA linear PRI 09-JAN-2002
Homo sapiens chromosome 18, clone RP11-635D8, complete sequence.
ACO91647
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-635D8 Unpublished
                                                                                                                                                             AC091647.4 GI:18093025
                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 173368)
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                                                                                                                                                                                                                                      Homo sapiens.
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AUTHORS
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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farc, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heafcord, A., Hotton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macthews, C., Macdonald, P., McKernan, K., McPheeters, R., Matthews, C., McCarthy, M., McEwan, P., McRernan, K., McPheeters, R., Meldrim, J., Norbu, C., Norman, C.H., Polnonell, P., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Schupback, R., Rawmond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Stenaer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M., Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 9, 2002 this sequence version replaced gi:15145252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP6 end overlaps AC011155 [WICGR project L2947; in finishing] by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T7 end overlaps AC019239 [WICGR project L1005] by 143942 bp. We will submit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entire L13183 clone [29426 bp unique unsubmitted a/o 8/4/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L13183
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Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC"
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Web site: http://www-seq.wi.mit.edu
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/note="<30 qual SNGL region"
817. .1019
/rpt_family="MIR"
1365. .145^
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2604. .2648
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2114, .2118
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/organism="Homo sapiens"
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1643. .1695
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1912. .1916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="18"
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repeat\_region

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16288 h
9054 h
9687 h
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3055
3831
                                                  DRAFT SEQUENCE, 41 unordered pieces.
                                                                     APO01484.2 GI:8117342
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-635D8.
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35342 contig of
35242 contig of
43767 contig of
60206 contig of
67220 contig of
73733 contig of
73733 contig of
91829 contig of
91829 contig of
107979 contig of
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107979
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25543
35330
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122476
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AUTHORS
   RESULT 58
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                                                /note="<30 qual SNGL region"
complement(3266. .3550)
/rpt_family="AluSq"
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complement(19374, .19719)
/rpt_family="L2"
20270. .20457
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/rpt family="WRR5A"
complement(20621..20696)
/rpt_family="L2"
20720..20757
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Matches 47; Conservative 0; Mismatches
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21715. .21750
/rpt_family="AT_rich"
complement(22572. .22616)
/rpt_family="MIR"
                                                                                                                                                                                              /rpt_family="MERSA"
complement(13365. .13568)
/rpt_family="MIR"
complement(14097. .14266)
/rpt_family="LiMA4A"
14917. .15064
                                                                                                                                                                                                                                                                  /rpt family="MIR"
complement (16054. 16296)
/rpt family="MIR"
complement (16317. 16458)
/rpt family="MIR3"
16563. 16623
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25648. .25770
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complement(25798. .25822)
/rpt_family="MIR"
                                                                               Complement (4643. 4797)
/rpt family="L2"
complement (4904. 7127)
/rpt family="L1P"
complement (8029. 8334)
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/rpt family="MIR"
/rpt_family="(TCTA)n"
2778. .2802
/rpt_family="AT_rich"
2920. .2932
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7906. .17936
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24483. .24510
                                                                                                                                                                                                                                                                                                                                             rpt_family="GA-rich"
6980. .17093
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complement(18341..189
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23819. .23846
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Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hpp.gsc.riken.go.jp/, Tel:81-42-778-9923, Pax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7288178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
    HTG 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AP001484 185479 bp DNA linear HTG 30-MAY.
Homo sapiens chromosome 18 clone RP11-635D8 map 18q21, WORKING
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Center project name: Humbraft18
Center project name: Humbraft18
Center clone name: RPI1-635D8
Center clone name: RPI1-635D8
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 172243 bases at least Q40
Consensus quality: 172243 bases at least Q30
Consensus quality: 176665 bases at least Q30
Unsert size: 181479; sum-of-contigs
Quality coverage: 5.04x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 185479)
Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 185,479 genomic DNA of 18q21
Published Only in DataBase (2000)
2 (bases 1 to 185479)
Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is
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6423 bp in length
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91829: contig of 5619 bp in length
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144761: gap of 1726 bp in length 100 bp 100 
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/db_xref="taxon:9606"
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144661: contig of
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168437 170911: contig of
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171012 173108: contig of
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/clone="RP11-635D8"
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ACCESSION VERSION KEYWORDS

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11123 85122: contig of 74000 bp in length
85123 85222: gap of 100 bp in length
85223 92356: contig of 7134 bp in length
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f 1223 bp in length
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9: gap of 100 bp
11022: contig of 3273 bp in length
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of 1008 bp in length
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/clone="RP23-401D18"
/clone=lib="RPCI-23 Female Mouse BAC"
/in. 2300
/note="sssembly_fragment
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/note="assembly_fragment"
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187228. .190519
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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106069. .128004
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2401. 3604
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   3605 3704: gap of
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                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 190519)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-401D18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 401 D 18

Center clone name: 401 D 18

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consenus quality: 18719 bases at least Q40
Consenus quality: 188683 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 190199
Quality coverage: 13.0 in Q20 bases; sum-of-contigs
Quality coverage: 13.0 in Q20 bases; sum-of-contigs
Mus musculus clone RP23-401D18, WORKING DRAFT SEQUENCE, 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seg.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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2301 2400: gap of 100 bp
2401 3604: contig of 1204 bp in length
                                                                                      AC099591.1 GI:16946040
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
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                                                                                                                                                                               Mus musculus
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DEFINITION
                                                                                                                                                                               ORGANISM.
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JOURNAL
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COMMENT

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51942 AAAGAAATHTTTTCCATCATTTTGTAGAAATTACTGTCATTTAGAAAATGTAAGTTTT 52001
                                                                                                                                                                                                                                          51882 TAGATAAAATATCCAACAACATATGATTCAACATAAAAACAATAGAAAAAGGAAAAAGGAAA 51941
                                                                                                                                                                                                                                                                                                                               93 CGCGATACAATTTGGGGTGGATTGGCAACAAAACTTCCTGTGACTAACAGGTCCATAGTTTT 152
                                                                                 Gaps
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TITLE
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                                                                                                                                                     HTG 17-AUG-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200512)
                                                                                                                                                                                                                                                                                                                                                                                     Andrew, R.

Direct Submission
Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hundrary@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 21, 2002 this sequence version replaced gi:22265574.

Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 199640 bases at least Q40
Consensus quality: 199960 bases at least Q30
Consensus quality: 200067 bases at least Q30
Insert size: 200112; sum-of-contigs
Insert size: 19999; 6.6% error; agarose-fp
Quality coverage: 11.88x in Q20 bases; sum-of-contigs Quality
coverage: 11.97x in Q20 bases; agarose-fp
                                                                                                                                                                     Mus musculus chromosome 4 clone RP23-33915, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
                                                                                                                                                                                                                 AL844585.5 GI:22416220
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOB.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently * Consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                     linear
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68978 83970: contig of 14993 bp in length
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/note-sasembly fragment:02211

fragment chain:1"

68978 . .83970

/note-sasembly fragment:00776

fragment chain:1"

84071 . .101123
                                                                                                                                                     DNA
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/db_xref="taxon:10090"
                                                                                                                                                     200512 bp
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AL844585/c
                                                                                                                                                                        DEFINITION
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Streptocarpus holstii GcyclA protein (GcyclA) gene, partial cds. AF208338
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/db xref="G1:8650372"
/db xraf="G1:8650372"
/translation="MLGFDKPSKTLDWLLTKSKVAIKDLVLTNKSSSSRSPSSPSECE
VALNDEAFQDGSCLL-PDSKRNSASTYRDPAQSASTLAKESRAKARARAREFTKEKLC
IKKLNESRNWNNNLFTSNSQPVLHCPITNEATATQQDL1QESSVIKRMLRHHQSFFGF
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Lamiales; Gesneriaceae; Streptocarpus.
1, (Dases 1 to 591)
Citerne, H., Moeller, M. and Cronk, O. C. B.
Diversity of cycloidea-like genes in Gesneriaceae in relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                    32847 CGAGCAAAGAACAAAAATTAATTAACAATGTCAGAATATTCTGATTTTGTAATATC 32788
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                                                                                                                                                                                                                                                                                                                                                                           61 CGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAAC 120
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Submitted (19-NOV-1999) Royal Botanic Garden Edinburgh, 20A
Inverleith Row. Edinburgh EH3 5LR, UK
Location/Qualifiers
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/note="assembly_fragment:04201
fragment_chain:1"
101224: .198044
/note="assembly_fragment:00213"
                                                                                                            sture 198145. .200512"
/note="assembly_fragment:03592"
55849 a 41861 c 43308 g 59094 t
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/product="Gcyc1A protein"
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/product="Gcyc1A protein"
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2 (bases 1 to 591)
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/gene= "Gcyc1A"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 876)
Adler,E., Hoon,M.A., Mueller,K.L., Chandrashekar,J., Ryba,N.J. and
                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J.P.
and Zuker, C.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 GACCAGTGCTATGATGTTGTATCTGCTTGGTCAGTGATGCCATGAGAAGATGGTGGAGG 581
                                255 AAGGGCTAAGGCAAGAGCAAGGGCTAGGGAAAGAACAAAGGAGAAACTGTGCATCAAGAA 314
                                                                 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
                                                                                                  315 GCTRAATGAATCCAGAAACATGAACAACAATCTGTTTACATCWAAYAGCCAACCTGTTCT 374
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15 ATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG
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Zuker,C.S., Adler,J.E., Ryba,N., Mueller,K. and Hoon,M.
T2r taste receptor family
Patent: WO 0118050-A 31 15-MAR-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US); THE THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
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A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="human T2R16, hGR16"
t 205 c 163 g 293 t
                                                                                                                                                                                                                                                       AX097725 876 bp
Sequence 31 from Patent WO0118050.
                                                                                                                                   135 TAACAGGICCATAGITITICACGACACTICCA 166
                                                                                                                                                                     TCACTGCCCCATAACTAATGAAGCTACTGCAA 406
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Matches 60; Conserv
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/product="candidate taste receptor T2R16"
/protein_id="AAF43912.1"
/db_xref="c1726825"
/db_xref="c1726825"
/translation="wPIOLIVPFMITYULESLTIIVQSSLIVAVLGREWLOVRRLMP
VDMILLSLGISRFCLOWASMINNFCSYFNLNYVLCNLTITWEFFNILTFWINSLLTVP
YCIKVSSFTHHIFLWHRWRILRLFPWILLGSLMITCVTIIPSAIGNYIQIOLLTWBEI
PRNSTYTDRALBYALVEVPTSYFLTIITIGTLFDRASLTKQIQHHSTGHCNPS
MKARFTALRSLAVLFIVFTVYFYFTIITIGTLFDRRCWLWVWEAFVYAFILMHSTST
MLSSFTLKRILKGKC"
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSM804441 2002 2954 bp mRNA linear PRI 12-JUL-2002 Homo sapiens mRNA; cDNA DKFZp313J1832 (from clone DKFZp313J1832). AL833130
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKRZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braunschweig/Germany) within the cDNA sequencing consortium of the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            /note="G protein-coupled receptor; PCR-derived sequence; similar to an interval in BAC AC006518"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone (DKFZp313J1832) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 CCAGGAACAGGATGAAAGGAATAACCAATGCAACTGTATGAGCCTGGA 533
                                                                                                                                                                                                                                                                                                    product="candidate taste receptor T2R16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.2;
Pred. No. 43
                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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/clone="DKFZp313J1832"
                         Submitted (21-JAN-2000) NIDCR,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
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55.6%;
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                                                                                                                                                                                                                                     map="12p13"
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Direct Submission
                                                                                                                       1. .876
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Best Local Similarity
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Submitted (04-DEC-2001) Production Sequencing Facility, DOE Joint
Benome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 31041)
DOE Joint Genome Institute and Stanford Human Genome Center.
/tissue_type="cDNA-collection"
/clone_lib="313 (synonym: hlcc2). Vector pTriplEx2; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
2887. .2892
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Submitted (27-MRA-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94599, USA
On Mar 27, 2002 this sequence version replaced gi:17298615.
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          1509 AATAAATAAAATGAAAAATTCACCAGATGGATTTAGCTGCAGATAACATACTGTGGAAGA 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1569 AAGGATCAGTGAATTTGAGGATAGATCAATGTAAACCATCCAAATCAAAGCACAGAGAAA 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC104114 31041 bp DNA linear PRI 27-MAR-
Homo sapiens chromosome 5 clone RP11-238E17, complete sequence.
                                                                                                                                                                                                                                                                                                              78 AATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                         138 CAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
                                                                                                                                                                                                                                                                   0; Gaps
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                  Ouery Match 15.1%; Score 31.2; DB 9; Length 2954; Best Local Similarity 53.2%; Pred. No. 45;
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.dot
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                 0; Mismatches
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/chromosome="5"
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                                                                                                                                             616 g
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DOE Joint Genome Institute.
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                                                                                                                                             459 C
                                                                                                                                                                                                                                                                 66; Conservative
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polyA_site
BASE COUNT 109
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PRI 16-APR-2002
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Submitted (11-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                           27888 TCCTATGTCCATTCCTGGGCCACAGATACTAAGGAAGCTGAAGTGACCATGAAAGCTATA 27947
                                                                                                                                                    27948 CCGGGTGATTTGCTTTTGGGAAAGATGGCTCCACATTGGTGTGGGAAAACTGATTCACAGA 28007
                                                                                                90 CAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGT 149
30 TTCTTGGTCAATTTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAG
                                                                                                                                                                                                                                                                                                                                                                      ACI14759 80436 bp DNA linear PRI 16-7
Homo sapiens BAC clone RP11-347K3 from 4, complete sequence.
AC114759
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Tomlinson,C. and Haakenson,W.
The sequence of Homo sapiens BAC clone RP11-347K3
Unpublished (2001)
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Contact: sapiens@watson,wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 80436)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Center project name: H_NH0347K03
                                                                                                                                                                                                                                                     Db 28008 ATTGTGGGGTTCTTACAAGG 28027
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                                                                                                                                                                                                    150 TITTCACGACACTICCAAGG 169
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Waterston, R.H.
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6 (bases 1 to 80436)
Waterston, R.
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5 (bases 1 to 80436)
Waterston, R.H.
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repeat\_region

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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
This sequence was finished as follows unless otherwise noted:
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mcherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-II human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-219G10, 2000 bp overlap, the clone sequenced to the right is RP11-756F10, 2000 bp overlap, Actual start of this clone is at base position 155040 of RP11-219G10; actual end is at base position 72504 of RP11-756P10.

Polymorphisms have been identified between AC011729, AC022189, and AC114759. Data fromAC011729 and AC022189 was used to finish this clone, AC114759.

## FEATURES

'organism="Homo sapiens" db\_xref="taxon:9606" chromosome="4" rpt\_family="MER2\_type' 159..1366 'rpt\_family="MER1\_type" /rpt\_family="MBR2\_type" 564. .1697 rpt\_family="MER2\_type' 092. .1158 /clone\_lib="RPCI-11"
6. .98
/rpt\_family="L1"
99. .408 Location/Qualifiers clone="RP11-347K3" /rpt\_family="L1" 1790. .1920 rpt\_family="Alu" 09. .742 /rpt\_family="Alu" 9947. .9999 /rpt\_family="MIR" 11556. .11710 'rpt\_family="Alu" 683. .5884 /rpt\_family="L1" /rpt\_family="L2" /rpt\_family="L2" 9410. .9696 rpt\_family="L1" rpt\_family="L2" .1563 .1090 .80436 repeat\_region repeat\_region

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2006. .22083
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4483. .14800
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32845. .33173
/rpt_family="ERVL"
33193. .33277
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88718. .28920
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3298. .13462
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                             rpt_family="L2"
2713. .13152
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76203. .26520
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Length 80436; DB 9; 15.1%; Score 31.2; I 47.9%; Pred. No. 52; Best Local Similarity Query Match

'rpt\_family="MIR"

repeat\_region

Page 74

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Stren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwith, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwith, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Conke, P., Coke, P., DeArellano, K., Diaz, J. S., Collymore, A., Cooke, P., DeArellano, K., Diaz, J. S., Collymore, A., Cooke, P., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand-Pierre, N., Grand, J., Anderson, B., Harford, A., Horton, L., Kain, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Lili, G., Locke, K., Macdonad, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., Mackernan, K., O'Donnell, P., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J., Veasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Volly, W. Viel, R., Voll, W., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Volly, W., Wilson, M., Wilson, W., Wilson, W., Wilson, W., Wilson, W., Wilson, W., Wyman, D., Ye, W., J., Volly, W., Wilson, W., Wyman, D., Ye, W., Wilson, W.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                Db 36532 GCCATACAAATACATTATCTTTGCCTTTTGCCTATTGGCAGAACTTGCAGTATTTGGTCA 36473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36412 CTTGTTTGAGCTTTAACCAAATTTCTAACAGACACTGGCCAAATCCTACCAAGTGAAAAA 36353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36472 GAGAAGAAAGGAAATGCATAAAACTAAAACAGCTGACCTTCAGGTTGCTTTTGAAAATCCGA 36413
                                                                                                                                                                                                                                                                                                                                                       67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 CCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAA 186
      0; Gaps
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0; Mismatches 98; Indels
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Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,R., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Voiel,R., Vo,A., Wilson,B., Wu,X., Myman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allow
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L6689
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1821 bp in length
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9144: gap of 100 bp
9967: contig of 823 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802: contig of 802 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 100 bp contig of 828 bp in length
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16488: contig of 818 bp in length
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17404: contig of 816 bp in length
04: gap of 100 bp
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Web site: http://www-seq.wi.mit.edu
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7226; cont
7 7326; gap of
7 8123; cont
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11002 11860: cont
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3562: conf
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1815 2634: cor
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6302: cor
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3074: gap of 100 bp 23900: contig of 826 bp in length 4000: gap of 100 bp 24831: contig of 831 bp in length 4931: gap of 100 bp 25747: contig of 816 bp in length 2647: gap of 100 bp 2667: contig of 820 bp in length
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contig of 821 bp in length
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contig of 821 bp in length
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                              18427: gap of 100 bp
19261: contig of 834 bp
19361: gap of 100 bp
20187: contig of 826 bp
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of 837 bp
                                                                                                                                                                                      24: gap of 100 bp
22055: contig of 831 bp
55: gap of 100 bp
22974: contig of 819 bp
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of 806 bp
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21124: contig
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Direct Submission

Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Nov 17, 2001 this sequence version replaced gi:16444672.

During sequence assembly data is compared as variations

buring sequence ascelloud these are annotated as variations

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: EMBL; 8w:,

SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP

database can be found attention on the wormproper than one plasmid with their source databases: Em: EMBL; 8w:

Attention of the continued of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94341 bp DNA linear PRI 16-NOV-2001 sequence from clone RPI1-9F19 on chromosome 10, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                    102 ATTIGGGIGGATIGGCAACAACTICCTGTGACTAACAGGTCCATAGTTTTTCACGACAC 161
                                                                                                                                                                                                        Gaps
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                                                                                                                       DB 2; Length 83905;
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51636 51735: gap of 100 bp
51736 52551: contig of 816 bp in length
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                                                                                             15.1%; Score ... 52; 57.0%; Pred. No. 52; ... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   Db 84342 AAGACCCTGTCTCAAAAAAAAAAAAAAAAACTATGCAAATAACTGTGAACTACTTAATT 84401
/clone_lib="RPCI-11.1"
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/note="Sequence from overlapping clone RP13-20H14
(AL360090). Assembly confirmed by restriction digest"
26408 a 21362 c 21315 g 25256 t
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 8, 2002 this sequence version replaced gi:17940907.
                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 56339 bases at least Q40
Consensus quality: 56339 bases at least Q30
Consensus quality: 61437 bases at least Q20
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gap of unknown length
gap of unknown length
contig of 110 bp in length
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contig of 108 bp in length
gap of unknown length
contig of 1338 bp in length
gap of unknown length
gap of unknown length
contig of 1266 bp in length
gap of unknown length
contig of 124 bp in length
gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-2L5
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379101 bp DNA linear HTG 16-AUG-2002
Mus musculus clone RP23-250M13, *** SEQUENCING IN PROGRESS ***, 19
ordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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contig of 4325 bp in length
gap of unknown length
contig of 7399 bp in length.
                                                                                                                                                                                                                                                                                      78; Indels
  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC113004.
AC113004.3 GI:22267719
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70076 TGTAAGGCTTCCTTAGTAGAAGACAACACTTCGCAG 70041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 ACTAACAGGICCATAGTITITICACGACACTICCAAG 168
                                                                                                                                                                                                                                                                                   0; Mismatches
  of 2754
                                                                                                                                                                                                                             Score 31.2; I
Pred. No. 53;
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-250M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110000
210000
310000
contig
gap of
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                                                     97118:
97218:
101543:
101643:
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50.0%;
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Best Local Similarity
Matches 78; Conserv
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AC113004_1
AC113004_2
AC113004_3
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REFERENCE AUTHORS

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Submitted (22-OCT-1999) Department of Genetics, Washington
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          Strenger 1 to 379101 Strength of the strength 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
Research, 320 Charles Street, Cambridge, MA 02141, USA
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------ Project Information
Center project name: L22543
Center clone name: 250_M_13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p of 100 bp contig of 19175 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58: gap of 100 bp
15766: contig of 37508 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5866: gap of 100 bp
154746: contig of 38880 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4846: gap of 100 bp | 190149: contig of 35303 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10249; gap of 100 bp 227757; contig of 72278 bp in length 77857; gap of 100 bp in length 235085; contig of 7228 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ap of 1900 bp contig of 19175 bp in length
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1 3547 contig of 3547 bp in length
3548 3647: gap of 100 bp
6293 6392: contig of 2645 bp in length
6293 6392: gap of 100 bp
6393 10971: contig of 4579 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254361 254460: gap of 100 bp
254461 258007: contig of 3547 bp in length
258008 258107: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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258008 258107: gap of
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154847 190149
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235186 25436
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PRI 21-FEB-2002
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Submitted (17-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 73440 ATATTAAGGAAGTATCATTCTTCTTTGGCAAATGCAAAAACCCTATGATTTGGCACTGA 73381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73380 AANTNGTTTTNATGAGTAATGGAGGGCATATCTTTACTGGGAATAGAATTCTAAATCTCT 73321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACACAGATGATTCGGTCCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC004838 142992 bp DNA linear PRI 21-FF
Homo sapiens PAC clone RP4-589D8 from 7q31.1-q31.3, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142992)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 31.2; DB 2; Length 110000; 49.7%; Pred. No. 53;
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Wohldmann, P., Graves, T., Sutterer, C. and Scherger, E.
The sequence of Homo sapiens PAC clone RP4-589D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="RP23-250M13"
/clone lib="RPC1-23 Female Mouse BAC"
/ 7076I c 70672 g 115769 t 2878 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              359827 359926: gap of 359927 379101: contig of 19175 bp in length. Location/Qualifiers
258108 295615: contig of 37508 bp in length 29516 295715: gap of 100 bp 102944 302043: contig of 7228 bp in length 302944 302043: gap of 100 bp 100 bp 322219 322218: gap of 100 bp 100 bp 322219 322218: gap of 100 bp 100
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Genome Res. 8 (11), 1097-1108 (1998)
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3 (bases 1 to 142992)
Waterston, R.H.
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Waterston, R.H.
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Waterston, R.
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Mashington University Genome Sequencing Center. For additional information about the map position of this sequence, see thtp://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                          Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 17, 1999 this sequence version replaced gi:3213159.
                                                                                               Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 142992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at http://www.chori.org using the mathod described by Ioannou et al., Nature Genetics 6:84-9 (1994).

The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com), or from Pieter de Jong.
   4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the right is DJ1166A24, 200 bp overlap. Actual start of this clone is at base position 1 of DJ0589D08, actual end is at 15237 of DJ1166A24.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_DJ0589D08
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/db_xref="taxon:9606"
/chromosome="7"
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1551. .1727
/rpt_family="MER1_type"
2256. .2339
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/rpt_family="CT-rich"
1079. .1383
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/clone="RP4-589D8"
/clone_lib="RPCI-4"
676. .763
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University, 4444 Fores
6 (bases 1 to 142992)
Waterston,R.
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TITLE
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family="Retroviral"
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2544. .22665
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33567, ,23778
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24334. .24365
/rpt_family="AT_rich"
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2563. 25895
/rpt_family="A10"
25896. 25945
/rpt_family="AT_rich"
                                        /rpt_family="MER1_type"
44777. .4559
                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_tamil,
15626. .15773
/rpt_family="GA-rich"
'10205
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/rpt_family="(TCTA)n"
35598. .25617
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19259. 19815
/rpt_family="L1"
19837. 19909
/rpt_family="(TA)n"
19975. 20862
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1211. .21368
                                                                                                                                                                                                                        rpt_family="AT_rich"
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2297, 100co
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5301. .15375
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1069. .21148
                                                                                                                                                                                                                                                                                 1404. .8472
rpt_family="(TA)n"
                                                                                                                                              rpt_family="(TA)n"
                                                                                                                                                                                                                                                                                                                                                rpt_family="(TC)n"
4331. .14644
                                                                                                                                                                                                                                             'rpt_family="MaLR"
7861. .8312
                                                                /rpt_family="MaLR"
4558. .4666
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22521. , ????
                                                                                             rpt_family="MaLR"
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/rpt_family="MIR"
3456. .4102
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5336. .15623
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5. .21178
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1357. .21593
          3456. .4102
/rpt_family="L1"
                                                                                                               /rpt_family="L2"
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                                                            .4559
                                    4248
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1156.
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Homo sapiens
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                                                                                                                                 Db 26777 AGTT 26774
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KEYWORDS
                                                                                                                                                                                          RESULT 73
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases I to 14454)

Chauhan, R.S., Durfee, T.J., Holt, J.R., Blattner, F.R. and Leong, S.A.

Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0073N20 BAC genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-APR-2002) Genome Center, Unversity of Wisconsin, 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 11607 GACCAGTGCTATGATGTTGTATCTGCTTGGTCAGTGATGCCATGAGAAGATGGTGGAGG 11548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 26897 ATTGCCATGATATTGATGACGTGATTTGTGAAGGAAAATAAAACTAAACAATTGTTTT 26838
                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
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    1144544
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                             15.1%; Score 31.2; DB 9; Length 142992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 11547 ccaggaacagargaaaggaaraaccaargcaacrgrargagccrgga 11500
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Finished but unannotated.
Location/Qualifiers
                                                                                 /rpt_family="AT_rich"
27880. .28409
/rpt_family="MER4-group"
28411. .28449
                                                                                                                                                                                                                                            rpt family="MER4-group" 0159. .30457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144544 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="OSJNBa0044D15"
31829 c 32746 g 39
                                                                                                                                                                                                                                                                                                                       /rpt_family="AT_rich"
                                                                                                                                               /rpt_family="(TTA)n"
38450. .29714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence, complete sequence.
                                                                                                                                                                                                                                                                            /rpt_family="Alu"
30673. .30710
                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                'rpt_family="L1"
                                                 /rpt_family="L1"
27713. .27759
               /rpt_family="L1"
26552. .26659
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2 (bases 1 to 144544)
                                                                                                                                                                                                                                                                                                                                                                             55.6%;
                                                                                                                                                                                                                                                                                                                                                                                               60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Matches 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                           Query Match
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TITLE
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AC022189.2 GI:7230131
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
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1704 3721: co
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                                                                             Homo sapiens
                                                                                                                                                                                        Unpublished
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JOURNAL
                                                                           ORGANISM
                                                                                                                                    REFERENCE
AUTHORS
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Homo sapiens chromosome 11 clone RP11-16M7 map 11, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 135109 GAGAAGAAGGAAATGCATAAAACTAAACAGCTGACCTTCAGGTTGCTTTTGAAAATCCGA 135050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 135049 CTTGTTTGAGCTTTAACCAAATTTCTAACAGACACTGGCCAAATCCTACCAAGTGAAAA 134990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 GCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCC 66
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                      69402 69501: gap of 100 bp 69502 100507: contig of 31006 bp in length 100508 100607: gap of 100 bp 100608 146118: contig of 45511 bp in length. Location/Qualifiers
                                                                                                                                                                                            30423 30522: gap of 100 bp 30523 50525: contig of 20003 bp in length
                                                                                                                                                                                                                                 50526 50625: gap of 100 bp
50626 69401: contig of 18776 bp in length
                                                                                                             13405 13504: gap of 100 bp
13505 21030: contig of 7526 bp in length
                                                        6179: contig of 6179 bp in length
                                                                             6180 6279: gap of 100 bp
6280 13404: contig of 7125 bp in length
                                                                                                                                                      p of 100 bp contig of 9292 bp in length
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1. .6179
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Pred. No. 53;
0; Mismatches
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note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="RP11-16L12"
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100608. .146118
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21131 30422: cont
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Best Local Similarity 47.9%;
Matches 90; Conservative 0
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ORIGIN
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AC022189/c
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, W., Beckerly, R., Beda, F., Chosepal, M., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Domino, M., Doyle, M., Galagan, J., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Farrent, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, M., Meneus, L., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnall, P., Olivar, T.M., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M., Willey, W., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Subramanian, A., Talamas, J., War, X., Wyman, D., Ye, W.J., Direct, Submission, M., Yiel, R., Wall, R., 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center clone name: 16 M 7
Center clone name: 15 M 7
Sequencing vector: M13; M77815; 100% of reads
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                                                                        Mammalia; Eutheria; Primates; Catarrhin; Homi:
1 (bases 1 to 146525)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-16M7
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vector side:left"
eature 124711. .146525
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43198 a 27635 c 28215 g 45968 t 1509 others
                                                                                                                                                                                                                                                                                                                              107070 107169: gap of 100 bp 107170 124610: contig of 17441 bp in length 124611 124710: gap of 100 bp 124711 146525: contig of 21815 bp in length.
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74818 90123: contig of 15306 bp in length
90124 90223: gap of 100 bp
90224 107069: contig of 16846 bp in length
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11586 11685: gap of 100 bp
11686 15735: contig of 4050 bp in length
15736 15835: gap of 100 bp
15836 20054: contig of 4219 bp in length
                                                                     20055 20154: gap of 100 bp
20155 28690: contig of 8536 bp in length
                                                                                                           28790: gap of 100 bp 35706: contig of 6916 bp in length
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/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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.Query Match 15.1%; Score 31.2; DB 2; Length 146525; Best Local Similarity 47.9%; Pred. No. 53; Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
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linear PRI 06-APR-2002
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5': RP11-699P13 (UWGC:djs721) AC083875 28316-bp clone overlap
3': RP11-191E5 (UWGC:djs366) AC009358 149649-bp clone overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153232)
                                                                                                                                                                        Db 142209 GAGAAGAAAHGCATAAAACTAAACGCIGACCTTCAGGTTGCTTTGAAAATCCGA 142150
                                                                                                                                                                                                                                                                                         Db 142149 CTTGTTTGAGCTTTAACCAAATTTCTAACAGACAGCTGGCCAAATCCTACCAAGTGAAAA 142090
                                                     Db 142269 GCCATACAAAATACATTATCTTTGCCTTTGCCTATTGGCAGAACTTGCAGTATTTGGTCA 142210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-JUL-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 153232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACO24086 153232 bp DNA linear PRI 06-APR-2
Homo sapiens chromosome 7 clone RP11-242F21, complete sequence.
ACO24086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-APR-2002) Genome Center, University of Washington, Box 35145, Seattle, WA 98195, USA On Apr 6, 2002 this sequence version replaced gi:9101975.
                                                                                                                67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
                                                                                                                                                                                                                                    127 CCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAA 186
7 GCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23.FEB-2000) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 153232)

Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
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Center clone name: RP11-242F21 (djs634)

------ Summary Statistics

Consensus quality: 153136 bases at least Q40

Consensus quality: 153233 bases at least Q40

Consensus quality: 153232 bases at least Q30

Consensus quality: 153232 bases at least Q20

Insert size: 153232; sum-of-contigs

Quality coverage: 11.5x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 153232)
Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
Direct Submission
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This entry has been annotated with sequence quality
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Center Code: UWGC
Web site: http://www.genome.washington.edu
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_----- Project Information
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Unpublished
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All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file. estimates computed by the Phrap assembly program.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

<1300 <1300 <1300 <1300 <1300 SeqDerMap FngrPrnt ECORI <1300 <1300 SeqDerMap FngrPrnt BglII <1300 <1300 SegDerMap FngrPrnt <1300 <1300 <1300 <1300 <1300 

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Query Match 15.1%; Score 31.2; DB 9; Length 153232; Best Local Similarity 53.2%; Pred. No. 53; Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps
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Db 50241 AATAAATAAAATGAAAAATTCACCAGATGGATTTAGCTGCAGATAACATACTGTGGAAGA 50300 78 AATAGAACTAAGCAACGCGATACAATTTGGGTGGGATTGGCAACAAACTTCCTGTGACTAA 137

Qy 198 TTAT 201

Db 50361 AAAT 50364

Search completed: February 15, 2003, 23:24:37 Job time: 3137.5 secs

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1565.980 Million cell updates/sec
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Sequence 6, Al
Sequence 1, Al
Sequence 3593
Sequence 1, Al
Sequence 1, Al
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/ cgn2_6/ptodate/l/pubpna/DSO7_PUBCOMB.seq:*

/ cgn2_6/ptodate/l/pubpna/DSO6_NEW_PUB.seq:*

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-91-980-2

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US-09-961-527A-1

US-09-978-199-1

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Listing first 100 summaries
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Sequence 565, App Sequence 892, App Sequence 4, Appli Sequence 355, App Sequence 3155, Ap Sequence 451, App Sequence 81, Appl Sequence 7, Appl Sequence 7, Appli Sequence 38, Appli Sequence 385, Ap Sequence 9, Appli Sequence 208, Appl Sequence 161, Appl Sequence 208, Appl Sequence 208, Appl Sequence 208, Appl Sequence 208, Appl Sequence 161, Appl 109, App 1, Appli 9, Appli Sequence 1, Appli Sequence 3995, Ap Sequence 989, App Appli Sequence 5349, Ap Sequence 3, Appli Sequence 16642, A Sequence 8383, Ap Sequence 415, App Sequence 5, Appli Sequence 939, App Sequence 5349, Ap 161, 161, Sequence 7, Sequence US-09-878-178-939
US-09-38-842A-5349
US-09-38-842A-5349
US-09-9864-761-16442
US-09-9864-761-16442
US-09-9864-761-16442
US-09-9864-761-16415
US-09-980-476-1916
US-09-980-476-1916
US-09-980-476-1916
US-09-980-476-1916
US-09-980-476-1916
US-09-980-482-109
US-09-981-752-181
US-09-981-752-181
US-09-991-864-761-396
US-09-991-864-761-3 9 1 000000000 1133 1507 2910 5772 58985 O

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0; Mismatches
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US-09-510-332-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.6%
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-09-393-634-65/c
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LENGTH: 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                             Welch, Rod TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 13213 TGGCCAATTTTCTGGACGAGAAGAATATGTCCTGGAAGACCCAGCCAATAGAAAAAACCG 13154
                                                                                  208,
                                                                    208,
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                                                     208,
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                                                                  Sequence 2
Sequence 2
Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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US-09-989-722-208
US-09-989-723-208
US-09-989-779-208
US-09-989-731-208
US-09-989-731-208
US-09-991-073-208
US-09-991-073-208
US-09-991-073-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 166:
                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DBC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            Sequence 166, Application US/10114170
Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                      Burland,
Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 166:
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STRANDEDNESS: double
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...cruICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adva, Mick
APPLICANT: Hool, Mark
APPLICANT: Hool, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278A1el Family of Taste Receptors
FILE REFERENCE: 02307E-098010US
CURRENT APPLICATION NUMBER: US 09/510,332
PRIOR PILLOGATION NUMBER: US 09/393,634
PRIOR FILLNG DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SSOFTWARE: Patentin Ver. 2.1
LENGTH: 876
TYPE: NW.
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Wick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: The Reversented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
CURRENT APPLICATION NUMBER: US/09/393,634
NUMBER OF SEQ ID NOS: 92
13153 ACAAAGTTATGGAGGCGCTTAAGGCTGCAACTACCCATGACTATGAAGTGTATAGCTTTG 13094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.1%; Score 31.2; DB 9; Length 876; 55.6%; Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Indels
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                                                                                                              Db 13093 CTAAAAATTATTCCCAGATGAAAGCGATCTGGTAGTTGTGTTA 13050
                                                       154 CACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
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RESULT 5
US-09-946-807-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 AAGGAGGGTTATGATTACTGGGTCGATGACGGTTAGATTGCCAATTCGACGGAGGAAAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACATTCCTGTGAC 134
                                                                                                                                                Gaps
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                                                                                  Gaps
                                                                                                                        5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
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                                      Query Match 15.1%; Score 31.2; DB 10; Length 876; Best Local Similarity 55.6%; Pred. No. 0.44; Matches 60; Conservative 0; Mismatches 48; Indels 0
                                                                                                                                                                                                        65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGA 112
                                                                                                                                                                                                                                               580 ccaccaacacarcaaaccaaraaccaarccaacrerarcaccroca 533
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 999
SOFTWARE: FRACSEQ for Windows Version 4.0
SEQ ID NO 917
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                  Sequence 917, Application US/09770791 Patent No. US20020062014A1
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; OTHER INFORMATION: n = A,T,C or G
US-09-770-791-917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis, Keith R.
Allen, Keith
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Slader, Ted
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Best Local Similarity
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US-09-393-634-65
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                           APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345_2004_001
CURRENY APPLICATION NUMBER: US/09/946,807
CURRENY FILING DATE: 2001_09_05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000_02_28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FRASESO FOR Windows Version 4.0
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
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INFORMATION: b=g or c or t/u
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OTHER INFORMATION: h=a or c or t/u
Sequence 1, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
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LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or
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OTHER INFORMATION: y=t/u or c
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LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
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OTHER INFORMATION: w=a or t/u
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INFORMATION: m=a or c
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Best Local Similarity 54.1
Matches 59; Conservative
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OTHER INFORMATION: r=g or
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OTHER INFORMATION: s=g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                         Db 504809 AGACGAATGGAAGACTACATTCTTTCTACTGACTGGTCATCGGTTTTTTC 504857
                                                                                  106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTC
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004.001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
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OTHER INFORMATION: d=a or g or t/u
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OTHER INFORMATION: h=a or c or c/u
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OTHER INFORMATION: v=a or g or
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NAME/KEY: misc feature
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OTHER INFORMATION: r=g or a
MAMB/KEY: misc_feature
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LOCATION: (1)...(1531)
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Db 504749 AGGCAAGTGGTGAATAGATCCAATAAAAATAAAAATAGAATAAGAATAAGAAGATAATA 504808
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                                      Db 504809 AGACGAATGGAAGACTACATTCTTTCTACTGACTGGTCATCGGTTTTTC 504857
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106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTC 154
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                                                                                                                                             US-09-195-686-1
Sequence 1, Application US/09795686
APPLICANT: Stefansson, Hreinn
APPLICANT: Guicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 09/515,715
FRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FASTERO FOR MINDOWS VErsion 4.0
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1
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NAME/KEY: misc_feature
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OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
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OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
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OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
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OTHER INFORMATION: 8=g or c
NAME/KEY: misc_feature
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OTHER INFORMATION: m=a or c
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OTHER INFORMATION: r=g or a
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Best Local Similarity 54.1%
Matches 59; Conservative
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Db 504749 AGGCAAGTGGTGAATAGATCCAATAAAATAAAAGAAATAGAATAAGAAGATAATA 504808

46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105

14.1%; Score 29; DB 10; Length 1503841; ilarity 54.1%; Pred. No. 53; Conservative 0; Mismatches 50; Indels 0;

Query Match Best Local Similarity Matches 59; Conserv

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50; Indels 0; Gaps

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0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PEDLICATION NUMBER: US/09/737484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2176, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-825-294-77
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Best Local Similarity 50.4%;
Matches 58; Conservative
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ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI
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OCHIAI, KEIKO
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SENOH, AKIHIRO
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US-09-738-626-2176
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                                         Sequence 9, Application US/09983965

Patent No. US2002013716041

Patent No. US2002013716041

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Patt, John C.

APPLICANT: Wattialagan, Nagappan

TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION

FILER REFERENCE: 37-21(1029)70

CURRENT APPLICATION NUMBER: US/09/983,965

CURRENT APPLICATION NUMBER: US 09/465,231

PRIOR APPLICATION NUMBER: US 60/113,678

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 5912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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LOCATION: 63, 66, 81, 83, 89, 107, 115, 118, 147, 151, 190, 232, 275,
LOCATION: 288, 294, 304, 323, 332, 369, 392
OTHER INFORMATION: n = A,T,C or G
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Fatent No. US20020173638A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesh, David Alan
APPLICANT: Molesh, David Alan
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 21011.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 28.6; DB 10; Length 339; 67.8%; Pred. No. 2.3; tive 0; Mismatches 19; Indels 0
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Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 58; Conservative 0; Mismatches 57; Indels
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US-09-970-966-77
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     RESULT 8
US-09-983-965-9
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74 GTTAAATNCNGGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATATA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GATACAATTTGGGTGGATTGGCAACAAAACTTCCTGTGACTAACAGGTCCATAGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 ACTACTATACAGGNGATNTGCAAAACCCCTACTGGGAAATCCATTTCATTAGTT 188
96 GATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTT 150
                                                            134 ACTACTÁTACAGGNGATNTGCAÁAAACCCCTACTGGGÁAATCCÁTTTCATTÁGTT 188
                                                                                                                                                 Sequence 77, Application US/09825294

Sequence 77, Application US/09825294

Patent No. US20020004491A1

SERERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Algare, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210.121.48462

CURRENT APPLICATION NUMBER: US/09/825,294

CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215

SOFTWARE: PASTERQ for Windows Version 3.0

FILE TOWER OF SEQ ID NOS: 215

SEQ ID NO 77
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Pred. No. 2.5;
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LENGTH: 3012
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Patent No. US20020142324A1
GENERAL INFORMATION:
APPLICANT: Wang, Xun
APPLICANT: Yoder, Olen
APPLICANT: Wu, Jianguo
TITLE OF INVENTION: Fungal target genes and methods to identify those genes
FILE REPERENCE: TW0129-UT
FILE REPERENCE: TW0129-UT
CURRENT APPLICATION NUMBER: US/09/961,527A
CURRENT FILING DATE: 2001-09-24
FRIOR APPLICATION NUMBER: US 60/234,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sinon, Andras
APPLICANT: Sinon, Andras
APPLICANT: Briksson, Ulf
APPLICANT: Dryja, Thaddeus P.
APPLICANT: Dryson, Eliot
APPLICANT: Dryson, Eliot
APPLICANT: Dryson, Eliot
APPLICANT: Berson, Eliot
APPLICANT: Berson, Eliot
APPLICANT: Berson, Eliot
TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis
TITLE OF INVENTION: Retinol
TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
FILE REPRENCE: LUD 5601
CURRENT APPLICATION NUMBER: US/09/991,980
PRIOR APPLICATION NUMBER: 09/880,427
PRIOR APPLICATION NUMBER: 09/880,427
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                             1598 GCATTACCCAGGGCATTGGTGCATACCAGGTCAAGGTAAATGTCGAGGACACTGACCGCA 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 28.2; DB 10; Length 6330; 64.6%; Pred. No. 11; tive 0; Mismatches 23; Indels 0;
                                                                                               13.8%; Score 28.4; DB 9; Length 3012; 60.3%; Pred. No. 6.8; Ative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHEN INFORMATION: nucleotide not determined
US-09-991-980-2
                    ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09991980 ; Patent No. US20020119543A1
                                                                                                                                                                                                                                                                                                                                              1658 CGATCACCTTCCTGGATA 1675
                                                                                                                                                                                                                                                                                                61 CGGTCCAAGAACAGGATA 78
                                                                                               Query Match 13.89
Best Local Similarity 60.39
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.64
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                              US-09-738-626-2176
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US-09-961-527A-6/C
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LENGTH: 6330
TYPE: DNA
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APPLICANT: Yoder, Olen
APPLICANT: Wu, Jianguo
TITLE OF INVENTION: Hungal target genes and methods to identify those genes
FILE REFERENCE: TM0129-UT
CURRENT APPLICATION NUMBER: US/09/961,527A
CURRENT PELING DATE: 2001-09-24
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/234,650
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 12487 CGTAGAAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCAACTGCTGTAGAT 12428
                                                                                                                                                                                                                                                                                                                                                                                                               5642 CGTAGAAGAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCAACTGCTGTAGAT 5583
                                                                                                                                                                                                                                                                                                                                                                20 CGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAA 79
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VECTORS AND VACCINES FOR FELINE
CALICIVIRUS DISEASE AND METHODS FOR
PRODUCING AND USING SAME
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5582 TAGAACTCCTCCTGAGAATCTTGCGAGGGAATTGAATCCAGC 5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 TAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 TAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.7%; Score 28.2; DB 10;
54.3%; Pred. No. 16;
tive 0; Mismatches 48;
                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                             Score 28.2; I
Pred. No. 12;
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/234,650
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09961527A
Patent No. USZ0020142324A1
; GENERAL INFORMATION:
APPLICANT: Wang, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09827864; Patent No. US20020009458A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             Query Match 13.7%;
Best Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.3;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                              57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Cochliobolus
                                                                                                                                                                                 ORGANISM: Cochliobolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-961-527A-1/c
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US-09-827-864-23/c
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                                                                                                                                  LENGTH: 8091
                                                                                                                                                                                                           US-09-961-527A-6
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                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                              Matches
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Query Match
13.4%; Score 27.6; DE
Best Local Similarity 51.4%; Pred. No. 4.9;
Matches 54; Conservative 0; Mismatches
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Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09978199
; Patent No. US20020104126A1
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 TGTGACTAACAGGTCCATAGTT 150
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Monahan, John E.
Schlegel, Robert
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Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1)..(441)
US-09-978-199-1
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US-09-879-536-653/c
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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: LOCATION: 108-109, 114, 117, 124, 133-134, 139, 141, 151, 161, 167, 176, 179, 185,

: OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-3559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: April 21, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.6%; Score 28; DB 10; Length 2007; Best Local Similarity 56.5%; Pred. No. 7.8; Matches 52; Conservative 0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700380551H1
                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                       STREET: 1850 K STREET, N.W., SUITE 500 CITY: WASHINGTON
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/827,864
FILING DATE: 06-Apr-2001
CLASSIFICATION **CURROWS**
ATTORNEY/AGENT INFORMATION:
NAME: GADIANO, WILHLEM F
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37712-213
TELEPHONE: (202) 778-8373
TELEPHONE: (202) 778-8373
  ADDRESSEE: MCDERMOTT, WILL & EMERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 CTGTGACTAACAGGTCCATAGTTTTTCACGAC 159
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-827-864-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 AAGTGGGGATCCCAGCCATAGTATTTAAGCAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3593, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2007 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERL Program
                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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LENGTH: 308
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APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR APPLICATION NUMBER: 60/240,967
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATCHIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 GCAAAGCATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGT 399
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DB 10; Length 308;
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                                                           Indels
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TILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                  132 GACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCAT 176
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Patent No. US20020156011A1

GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Heather
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARER FEASTGE FEASTGE FOR Windows Version 4.0
                                                                                                                                                                                                                         Length 468;
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13.4%; Score 27.6; DB 9; Length 500;
Best Local Similarity 56.7%; Pred. No. 6;
Matches 51; Conservative 0; Mismatches 39; Indels
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Patent No. US2002017552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
                                                                                                                                                                                                                                                                     44; Indels
                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.1%; Pred. No. 5.8;
Matches 54; Conservative 0; Mismatches 44;
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                 NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 1998-06-10
                                                                                                                                          ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                  SEQ ID NO 653
LENGTH: 468
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                                                                                                                     TYPE: DNA
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APPLICANT: Kreps, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wann
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/24, 647
PRIOR APPLICATION NUMBER: US 60/300,111
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                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 27.6; DB 9; Length 500; 56.7%; Pred. No. 6;
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                            CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/878,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GCGATACAATTTGGGTGGATTGGCAACAAA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5349, Application US/09938842A; Patent No. US2002160378A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(500)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 56.73
Matches 51; Conservative
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                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
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US-09-878-178-939
                                                                                                                    SEQ ID NO 939
LENGTH: 500
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PRIOR APPLICATION NUMBER: US 60/180,312
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Patent No. US20020048763A1
GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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-09-864-761-8383
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wenshay
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REPERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 21;
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CURRENT PELLING DATE: 2001-05-23

PRIOR PELLING DATE: 2001-05-23

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-06-03

PRIOR PELLING DATE: 2000-06-03

PRIOR PELLING DATE: 2000-06-03

PRIOR PELLING DATE: 2000-09-07

PRIOR PELLING DATE: 2000-09-07

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
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58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-16642
                                                                                                                                                                                                                                                                                                                   LENGTH: 10132
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                                                                                                                                                                                                                                                                                SEQ ID NO 3
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-K.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 TGCCGAGTTACTGGGAGCTGTAAGTTCCGGTCAAACCAGACCAGATGAGAACCATAAAAC 422
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OTHER INFORMATION: MAP TO AC007869.1
CTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.87
US-09-864-761-16642
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE Annowax Sequence Listing Engine vers: 1.1
SEQ ID NO 16642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.3%; Score 27.4; DB 10; Best Local Similarity 57.6%; Pred. No. 6.9; Matches 49; Conservative 0; Mismatches 36;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR PELING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
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RENKONEN, Risto
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Best Local Similarity
Matches 50; Conserv
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                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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| Sequence 415. Application US/09867701
| Sequence 415. Application US/09867701
| SERERAL INFORMATION:
| APPLICANT: Aglate, Paul A. |
| APPLICANT: Harlocker, Susan L. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND INSTRUMENT APPLICATION NUMBER: US/09/867,701
| CURRENT FILING DATE: 2001-05-29
| NUMBER OF SEQ ID NOS: 10912
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; Score 27.4; DB 10; Length 586; ilarity 55.9%; Pred. No. 7.5; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%; Score 27.2; DB 10; Length 391; 72.9%; Pred. No. 7.4; tive 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CCACCTTCCTGTGGCTAACAAGTTCCTTGATTTTCAATACAGATGCAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 CAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAA 167
                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1 OTHER INFORMATION: EXPRESSED IN BRARY, SIGNAL = 3.1
                   PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION UNMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GAACTAAGCAACGCGATACAATTTGGGTGGATT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 TCAGTAACCAAGTCATCCTTTGGGGTAAAAT 360
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AL158845.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; . LOCATION: (1)...(391)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 35; Conservative
                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 52; Conserv
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Best Local Similarity
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US-09-867-701-415
                                                                                                                                                                       SEQ ID NO 8383
TRNGTH: 586
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US-09-962-805-5
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APPLICANT: RAEBINAE, JArkko
TITLE OF INVENTION: USE OF RECOMBINANT ENZYMES FOR PREPARING GDP-L-FUCOSE AND FUCOSYL
TITLE OF INVENTION: GLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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APPLICANT: Anand, Naveen N.
TITLE OF INVENTION: GENES ENCODING MYCOBACTERIAL PROTEINS ASSOCIATED WITH
TITLE OF INVENTION: CELL BINDING AND CELL ENTRY AND USES THEREOF
TITLE OF INVENTION: CELL BINDING AND CELL ENTRY AND USES THEREOF
TITLE OF INVENTION: CELL BINDING AND CELL ENTRY AND USES THEREOF
CURRENT APPLICATION NUMBER: 1038-1231 MIS
CURRENT FILING DATE: 2002-06-24
PRIOR PELICATION NUMBER: 08/677,970
PRIOR FILING DATE: 1966-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2148 AACATAACATATCTTTTAAGCTTTTCTATCTTTTTGGAAATTTGGACCAATAAAATTCT 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2208 AGGIGAIATIGGAGGAIGGIAITGCICAACTICICAIAGIGAGACACCCCGIACAAAACA 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 CGATACAATTTGGGTGGATTGGCAACAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%; Score 27.2; DB 9; Length 4739; 56.8%; Pred. No. 21; tive 0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%; Score 27.2; I Best Local Similarity 50.8%; Pred. No. 19; Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2242/50463
CURRENT PAPLICATION NUMBER: US/09/962,805
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FI 20002114
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/10176640
; Publication No. US20030023056A1
; GENERAL INFORMATION:
                                                                                KALLIOINEN, Tuula
KAURANEN, Sirkka-Liisa
JAERVINEN, Nina
                      HIRVAS, Laura
HORTLING, Solveing
                                                                                                                                                                                 MAEKI, Minna
NIITTYMAEKI, Jaana
MATTILA, Pirkko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc feature

) LOCATION: (2492)...(2492)

; OTHER INFORMATION: unknown

US-09-962-805-5
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SEQ ID NO 1
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298 GGTCCCAGAAGGAGAGAGAGAAAGAAGAAGAAGATTATTTGAGAAACAATGCCTAAA 357
                                           62 GGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 TITCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 26.6; DB 10; Length 598; 50.4%; Pred. No. 14; tive 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
TITLE DE PROBREME: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                              ; Sequence 989, Application US/09770149
; Patent No. US20020059663A1
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GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth
APPLICANT: McCOy, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                  An, Yong-Olang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, Keith R.
Allen, Keith
Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                122 AACTICC 128
                                                                                                                                                                                           358 AACTICC 364
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                                                                                                                                                                                                                                                                                                        US-09-770-149-989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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APPLICANT:
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                                                                                                                                                                                                                                                       Sequence 3995, Application US/09864761

Ratent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Renk, David R.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
146 CGTTACAATTTCTGTCGATTTTCCCTTCTCTCGTGAAACCAGCTGAIGCAGAACGTCTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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13.1%; Score 27; DB 10; Length 460;
Best Local Similarity 62.7%; Pred. No. 9.3;
Matches 42; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: MAP TO AL049835.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
US-09-864-761-3995
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SOFTWARE: Annomax Sequence Listing Engine vers, 1.1
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CURRENT PEDILICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-09-37
PRIOR PELING DATE: 2000-09-37
PRIOR PILING DATE: 2000-09-37
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
                                                                              155 ACGACACTTCCAAGGACGCCATACCGAA 182
                                                                                                                                  86 TCAACATTCACACAGGCGCCGTAGCGCA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    US-09-864-761-3995
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FILING DATE: 2000-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TICCIGIGACIAACAGGICCAIAGITITICACGACACTICCAAGGACGCCAIACCGAACA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: DOLIVULEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTHARE: PATENTIN VET. 2.0
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TITLE OF INVENTION:

PLICE OF INVENTION:

Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION:

Nucleic Acids, Proteins, and Antibodies

CURRENT APPLICATION NUMBER: US/09/989,442

CURRENT FILING DATE: 2001-11-21

PRIOR PELING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/225,447

PRIOR APPLICATION NUMBER: 60/217,496

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/215,757

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14
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12.9%; Score 26.6; DB 9; Length 1.
Best Local Similarity 60.3%; Pred. No. 19;
Matches 44; Conservative 0; Mismatches 29; Indels
                                                                               Merberg, David
Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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US-09-989-442-81/c
Sequence 81, Application US/09989442
Publication No. US20030013649A1
GENERAL INFORMATION:
                                   Collins-Racie, Lisa A.
Evans, Cheryl
             LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                 Resnick, Richard J.
                                                                                                                                                                                                                                                                                                Fechtel, Kim
Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1033 GAGAAAAGAATAA 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-822-846-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 451
LENGTH: 1133
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/251,866
PRIOR FILING DATE: 2000-12-08
PRIOR PEDLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-0-09
PRIOR FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PELING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR PELING DATE: 2000-09-01
PRIOR PELING DATE: 2000-09-01
PRIOR PELING DATE: 2000-09-01
PRIOR PELING DATE: 2000-09-05
PRIOR PELING DATE: 2000-09-05
PRIOR PELING DATE: 2000-09-05
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR PAPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
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PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-11
PRIOR PILING DATE: 2000-09-11
PRIOR PILING DATE: 2000-09-11
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-17
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-10-20
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R APPLICATION NUMBER: 60/249,214
R APPLICATION NUMBER: 60/249,214
R APPLICATION NUMBER: 60/249,297
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/232,400
RR FILING DATE: 2000-99-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R APPLICATION NUMBER: 60/249,244

R FILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,217

R PILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,211

R FILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,215

R R PILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,264

R APPLICATION NUMBER: 60/249,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/226,681
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,759
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213
                                                                                                                           FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/239,935
FILING DATE: 2000-10-13
APPLICATION NUMBER: 60/239,937
FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                     FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,474
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/246,532
FILING DATE: 2000-11-08
                        FILING DATE: 2000-10-02
APPLICATION WUMBER: 60/237,040
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/240,960
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILING DATE: 2000-08-14
PPLICATION NUMBER: 60/227,182
ILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/235,836
APPLICATION NUMBER: 60/237,037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELICATION NUMBER: 60/249,218
LING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICATION NUMBER: 60/249,208
ILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICATION NUMBER: 60/249,213
ILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICATION NUMBER: 60/249,212
ILING DATE: 2000-11-17
PPLICATION NUMBER: 60/249,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILING DATE: 2000-11-17
PPLICATION NUMBER: 60/249,245
ILING DATE: 2000-11-17
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FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/241,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/225,214
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Sequence 88, Application US/09842552

Batent No. US/0020055628A1

GENERAL INFORMATION:

TITLE OF INVENTION: MULTILOCUS REPETITIVE DNA SEQUENCES FOR GENOTYPING BACILY

TITLE OF INVENTION: RELATED BACTERIA

FILE REFERENCE: S. 89,687

CURRENT APPLICATION NUMBER: US/09/842,552

CURRENT PILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/199,911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1365 AGATGAATCTTCTCAAGAGCAACAGAATCATTCTAAGCAAGACGACTCCGATCAGGGGCA 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AGAIGATICGGICCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTIGGGIGGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 1507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 21;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
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12.9%; Score 26.6; DE
Best Local Similarity 60.3%; Pred. No. 28;
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26.6;
Pred. No. 21
                                                                                                                                               R APPLICATION NUMBER: 60/33,063
RR FILING DATE: 2000-09-14
RR APPLICATION NUMBER: 60/232,397
RFILING DATE: 2000-09-14
RR PELLING DATE: 2000-09-14
RR FILING DATE: 2000-09-14
RR APPLICATION NUMBER: 60/232,401
RR APPLICATION NUMBER: 60/241,808
RR APPLICATION NUMBER: 60/241,808
R APPLICATION NUMBER: 60/241,808
R APPLICATION NUMBER: 60/241,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,065
FILING DATE: 2000-09-14
                                                                           APPLICATION NUMBER: 60/233,064
FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/241,826
FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/241,786
FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,475
       APPLICATION NUMBER: 60/231,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/241,221
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 88
LENGTH: 2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.9%;
Best Local Similarity 58.0%;
Matches 47; Conservative
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CRGANISM: Bacillus anthracis
US-09-842-552-88
                                   TILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TTGGCAACAACT 125
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PRIOR

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1305 ACAGCAACACTCT 1293

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Sequence 3, Application US/09901152
Publication No. US20030022824A1
GENERAL INFORMATION
SEQUENCE 3.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLO01248
CURRENT APPLICATION NUMBER: US/09/901,152
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                       APPLICANT: Yang, Yonghong
APPLICANT: Ang, Yonghong
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Weng, Jian Wai
APPLICANT: Weng, Jian Wai
APPLICANT: Weng, Along J.
TILLE OF INVENTION: No. US20020142302A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US20020142302A1 Yet Assigned
TITLE APPLICATION NUMBER: US/09/783,066
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: No. US20020142302A1 Yet Assigned
PRIOR PILING DATE: 2001-01-26
PRIOR PRILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PF.F.genes Version 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.9%; Score 26.6; DB 10; Best Local Similarity 58.0%; Pred. No. 37; Matches 47; Conservative 0; Mismatches 34;
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                    Sequence 7, Application US/09783066
Patent No. US20020142302A1
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                                                                                             APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
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LOCATION: (1)...(58985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: CDS
; LOCATION: (86)..(2125)
US-09-783-066-7
                                                                        GENERAL INFORMATION:
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ORGANISM: Human
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LENGTH: 58985
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.09-783-066-7/c
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APPLICANT: Penn, Sharron G.
APPLICANT: Fark, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hone, Weshers G.
ITILE OF INVENTION: HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GROWER: US (0/180, 312)
PILE REPREBACE: Abomica-K-1
CURRENT PILLNG DATE: 2001-05-20
CURRENT PILLNG DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILLNG DATE: 2000-05-26
PRIOR PILLNG DATE: 2000-05-26
PRIOR PILLNG DATE: 2000-05-36
PRIOR PILLNG DATE: 2000-06-36
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILLNG DATE: 2000-06-30
PRIOR PILLNG DATE: 2000-06-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PILLNG DATE: 2000-10-30
PRIOR
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                                                                12.9%; Score 26.6; DB 9; Length 58985; 56.2%; Pred. No. 97; ive 0; Mismatches 39; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 46030 CACAAAAGCAGAATAGAATGAGACAAAGC 46002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3985, Application US/09864761
Patent No. US20020048763A1
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                                                                        Query Match
Best Local Similarity
Matches 50; Conserv
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US-09-901-152-3
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Barent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PAPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775
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                                                                                                                    Gaps
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                                                                  Query Match 12.8%; Score 26.4; DB 10; Length 470; Best Local Similarity 54.0%; Pred. No. 15; Matches 54; Conservative 0; Mismatches 46; Indels 0;
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gane Logic, Inc.
ITILE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 4921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR PILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4 US-09-864-761-3985
                                                                                                                                                                                                                                                    126. TCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCC 165
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12.7%; Score 26.2; DE
Best Local Similarity 60.6%; Pred. No. 14;
Matches 43; Conservative 0; Mismatches
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; ORGANIEM: Glycine max
; OTHER INFORMATION: Clone ID: 701069758H1
US-09-878-574-15183
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APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark
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LENGTH: 282
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329 GGTTCCTTGCTTTTCACAACTCTCTCCAGGACGAAACTCTTCAGAGAAGGGGGTGGGA 388
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NAME/KEY: misc_feature
LOCATION: (1)._(510)
CTHER INFORMATION: n = a or c or g or t
US-09-917-800A-565
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Best Local Similarity 63.5%; Pred. No. 18;
Matches 40; Conservative 0; Mismatches 23; Indels 0
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TITLE OF INVENTION: Molecular Toxicology Modeling
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CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR PAPLICATION NUMBER: US 60/222,040
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 60/220,880
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR PILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR PELLING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-07-09
NUMBER: PALABLICATION NUMBER: US 60/303,459
PRIOR PILING DATE: 2001-07-09
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Patent No. US20020119462A1
GENERAL INFORMATION:
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Towis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
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US-09-917-800A-892
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LENGTH: 510
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SOFTWARE: Patentin Ver. 2.1

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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: True or Invention: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTT 126
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                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 26.2; DB 10; Length 1630; 63.5%; Pred. No. 30; ive 0; Mismatches 23; Indels 0;
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                                                                           NUMBER OF SEQ ID NOS: 370
SOSTWARE FRAUSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 1630
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                        TYPE: DNA ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 49; Conserv
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nes 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 42
US-10-067-385-7
                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
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Patent No. US20020115078A1

GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold

APPLICANT: Al-Garawi, Amal

APPLICANT: Miller, Charles

APPLICANT: Tomb, Jean-Francois

APPLICANT: Tomb, Jean-Francois

APPLICANT: Ownen, Raymond P.

TITLE OF INVENTION: Identification of Polynucleotides

TITLE OF INVENTION: Genome

FILE REPERENCE: 66132/041002

CURRENT APPLICATION NUMBER: US/09/881,752A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
                                                                                                                                                                                                                                                                                                                           28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTA 87
                                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1171229 US-09-917-800A-892
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                                                                                                                                                                                                                       Length 570;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                 Match 12.7%; Score 26.2; DB 10; Local Similarity 54.7%; Pred. No. 19; les 52; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: a, c, t, g, other or unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 rectregegaaarcciccaeerecticrecaaaa 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SMITH, JOHN C.
TITLE OF INVENTION: DIAGNOSTIC METHOD
FILE REPERENCE: PLS/00901/0277123
CURRENT APPLICATION NUMBER: US/09/778,900A
CURRENT FILING DATE: 2001-02-08
FRIOR APPLICATION NUMBER: GB 0004232.5
FRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 AAAAAAAGAAGAAAGAAGAAGACGAAA 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09778900A, Publication No. US20020192647A1; GENERAL INFORMATION:
                                                                                 ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.38
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-881-752A-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-778-900A-4
     SEQ ID NO 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEO ID NO 4
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                                                       TYPE: DNA
                                                                                                                                                                                                                       Query Match
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Matches
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RESULT 45
US-09-739-451-9
Sequence 9, Application US/09739451
Settent No. US20010024813A1
GENERAL INFORMATION:
APPLICANT: EDNEY. Reinhard
TILLE OF INVENTION: Dendriac and Brainiac-3
FILE REFERENCE: PP464
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CURRENT FILING DATE: 200-12-19
PRIOR APPLICATION NUMBER: 09/213,364
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: 60/077,687
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATCHTIN VOR: 2.0
                                                                                                                                                                                                                                    Sequence 1, Application US/09905119; Patent No. US20020096A1; GENERAL INFORMATION: APPLICANT: Murdin, Andrew D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 ACCAAGCTAGGTTTTTTTCC 1004
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                                                 2511 AGAGCAAACCAAGGGGACA 2529
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oomen, Raymond P. APPLICANT: Dunn, Pamela L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (101)..(1366)
US-09-905-119-1
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                           RESULT 44
US-09-905-119-1/c
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10272.147
CURRENT APPLICATION WUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION WUMBER: US 99/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 4440
SOFFWARE: PATENTI VERSION 3.0
SEQ ID NO 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 ACAATTIGGGIGGAITGGCAACAACTICCIGIGACIAACAGGICCAIAGITITITCACGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 ACACTTIGAAATTCTIGGAAAGATAAGTAATGTTTCTAAAAATGCCAAGGTATATTATGG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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APPLICANT: Choi, Gil
TILLE OF INVENTION: Streptococcus Pneumoniae Proteins and Vaccines
FILE REFERENCE: 469201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580201-580
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12.7%; Score 26.2; DB 12; Length 2319;
Best Local Similarity 53.4%; Pred. No. 34;
Matches 55; Conservative 0; Mismatches 48; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 CACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
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Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-067-385-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Saccharomyces cerevisiae US-09-801-368-109
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hothtzman, Doug
APPLICANT: Madden, Kevin
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Best Local Similarity 58.29
Matches 46; Conservative
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Sherman, Amir
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Milne, Todd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2319
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APPLICANT:
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TITLE OF INVENTION: Chiamydia Antigens and Corresponding DNA Fragments and TITLE OF INVENTION: Chiamydia Antigens and Corresponding DNA Fragments and TITLE OF INVENTION: Uses Thereof FILE REFRENCE: 1921-0.00 DIV CURRENT APPLICATION NUMBER: US/09/905,119 PRIOR APPLICATION NUMBER: 60/106,037 PRIOR FILING DATE: 1998-10-28 PRIOR FILING DATE: 1999-09-20 PRIOR FILING DATE: 1999-09-20 PRIOR APPLICATION NUMBER: 09/427,501 PRIOR APPLICATION NUMBER: 09/427,501 PRIOR APPLICATION NUMBER: 09/427,501 PRIOR SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1085 AACGTACTGTGGCAGACCAGTCTCCAGCTTTTCTGAGTCCCCCTAAAGTTCCTCCAATAA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AACTICCIGIGACTAACAGGICCATAGITITITCACGACACTICCAAGGACGCCATACCGA 181
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.6%; Score 26; DB 10; Length 1550; Best Local Similarity 57.3%; Pred. No. 34; Matches 47; Conservative 0; Mismatches 35; Indels
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                                75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACAACTTCCTGTGAC 134
                                                                                                 135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-12-24
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/08450
PRIOR FILING DATE: 1998-04-28
PRIOR PELING DATE: 1998-05-07
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PRIOR FILING DATE: 1997-06-16
PRIOR PLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Ferrara, Napoleone
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
65; Conservative
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                                                                                                                                                                        195 TTATTATCCT 204
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/08861
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088824
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LICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088212
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                                                FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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PPLICATION NUMBER: 60/090355
ILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/092182
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PRIOR FILING DATE: 1998-06-19
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                                                                                                           75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
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R FILING DATE: 1997-10-17
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R FILING DATE: 1997-11-12
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FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/087609
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-03-20
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                                      65; Conservative
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Napier, Mary A.
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Eaton, Dan L.
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   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               195 TTATTATCCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                709 GCATTGTCCT 718
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APPLICANT: Ashkenaz
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US-09-989-293A-208
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                                          Matches
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Query Match

R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/088029
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030
F FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-11
APPLICATION WINDER: 60/089105
APPLICATE: 1998-06-12
APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 APPLICATION UNMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 60/089532 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/088810 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088861 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-10 FILING DATE: 1998-06-16 FILING DATE: 1998-06-04 1998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 1998-06-17 FILING DATE: 1998-06-17 1998-06-17 DATE: 1998-06-02 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: PRILICA PRILIC PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 PAPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION UNDRER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090252 1998-06-26 FILING DATE: 1998-06-25 1998-06-22 FILING DATE: 1998-06-24 1998-06-25 1998-07-02 FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2739011C11 CURRENT APPLICATION NUMBER: US/09/989,735 CURRENT FILING DATE: 2001-11-19
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PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PRING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-12
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/075945
PRIOR PAPLICATION NUMBER: 60/075945
PRIOR PLING DATE: 1997-11-24
PRIOR PLING DATE: 1998-03-25
PRIOR PAPLICATION NUMBER: 60/08100
PRIOR PLING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
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PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-05
PR
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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                   Gerritsen, Mary E
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Napier, Mary A.
                                                                        Goddard, Audrey
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230RLC1
CURRENT APPLICATION UNMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
                                                                                                          75 GATAATAGAACTAAGCAACGGGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
                                                                                                                                                         135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGAAGGTG 194
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                                                                   Gaps
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Query Match 12.6%; Score 26; DB 9; Length 2095; Best Local Similarity 50.0%; Pred. No. 39; Matches 65; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.6%; Score 26; DB 9; Length 2095; Best Local Similarity 50.0%; Pred. No. 39; Matches 65; Conservative 0; Mismatches 65; Indels
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
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Publication No. US20020193299A1
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Publication No. US20020182638A1
GENERAL INFORMATION:
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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; ORGANISM: Homo Sapien
US-10-063-547-35
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LENGTH: 2095
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089952
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                                                  FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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                         APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-10
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75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAATTCCTGTGAC 134
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12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels
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Publication No. US20020193300A1
GENERAL INFORMATION.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Besteein, David
APPLICANT: Besteein, David
APPLICANT: Bestoopers, Luc
APPLICANT: Eaton, Dan L.
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RRIOR FILING DATE: 1998-07-02
RRIOR PELCATION NUMBER: 60/091544
PRIOR PELCATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
RRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/090678
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
                  APPLICATION NUMBER: 60/090535
                                    FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090690
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ING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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APPLICANT:

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PRIOR PAPLICATION NUMBER: 60/08855
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-09
PRIOR PELLING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088742
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLOATION NUMBER: 60/08824
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLOATION NUMBER: 60/08824
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-11
PRIOR PELLING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-17
PRIOR PELLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/09025
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR PELING DATE: 1997-06-17

PRIOR PELING DATE: 1997-06-16

PRIOR PELING DATE: 1997-01-17

PRIOR PELING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PELING DATE: 1999-11-24

PRIOR PELING DATE: 1999-11-24

PRIOR PELING DATE: 1999-11-24

PRIOR PELING DATE: 1999-02-25

PRIOR PELING DATE: 1999-02-25

PRIOR PELING DATE: 1998-02-05

PRIOR PELING DATE: 1998-03-20

PRIOR PELING DATE: 1998-03-20

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PRIOR PELING DATE: 1998-03-20

PRIOR PELING DATE: 1998-05-28

PRIOR PELING DATE: 1998-06-07

PRIOR PELING 
                                                                                                                                   Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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                                                                       Goddard, Audrey E.
                                                  Gerber, Hanspeter
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C69
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PRIOR PAPLICATION NUMBER: 60/065250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-05-27
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PRIOR PELING DATE: 1998-06-07
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APPLICATION NUMBER: 60/088212
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                                                                                                                  Godowski, Paul J.
Grimaldi, J. Christopher
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
  Ferrara, Napoleone
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                                               Gerber, Hanspeter
Gerritsen, Mary E.
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Napier, Mary A.
                                                                                             Goddard, Audrey
                          Pong, Sherman
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                R APPLICATION NUMBER: 60/090472
RR FILING DATE: 1998-06-24
RR APPLICATION NUMBER: 60/090535
RF FILING DATE: 1998-06-24
RR APPLICATION NUMBER: 60/090540
RFILING DATE: 1998-06-24
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Publication No. US20020197674A1
GENERAL INFORMATION:
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FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-07-07
PRIOR PELLING NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/090557
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/091478
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-06-24
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Betsonyers, Luc
APPLICANT: Baton, Dan L.
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Matches 65; Conservative
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
LING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
                                             FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090355
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                          APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACAACTTCCTGTGAC 134 589 GATGTGAAAGCCAGGCCAGTAGAGTTACTTGGGGTGAAAAAAAGTCTTGGTGGGGA 648 135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194 649 TATGAGGITCTTACATITITCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708 0 12.6%; Score 26; DB 9; Length 2095; 50.0%; Pred. No. 39; ive 0; Mismatches 65; Indels Sequence 208, Application US/09990436; Publication No. US20020198148A1
CENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 60/090445 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-06-25 1998-06-25 FILING DATE: 1998-07-07 FILING DATE: 1998-07-01 FILING DATE: 1998-07-01 Query Match
Best Local Similarity 50.09
Matches 65; Conservative -90-866 709 GCATTGTCCT 718 195 TTATTATCCT 204 FILING DATE: US-09-990-436-208 RESULT 52 PRIOR 엄 g ò g ò ò

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APPLICATION NUMBER: 60/088212
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FITLE OF INVENTION: Acids Encoding the Same FLLE REFERENCE: P2730HEBB: US/09/990,436
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/049787

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

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PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-04-28

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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                           Ferrara, Napoleone
Fong, Sherman
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Gerritsen, Mary E.
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Napier, Mary A.
   Eaton, Dan L.
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PRIOR AFFLICATION NUMBER: 60/086217
PRIOR PLING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
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PRIOR PLING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/088176
PRIOR PLING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR PLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19 PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
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PRIOR APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 1998-06-16

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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT FILING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PLING DATE: 1997-06-16
PRIOR PELICATION NUMBER: 60/062260
PRIOR PELICATION NUMBER: 60/065181
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-04-28
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Gurney, Austin L.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Goddard, Audrey
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                                           PRIOR PELLING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090472

PRIOR PELLING DATE: 1998-06-24

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PRIOR FILING DATE: 1998-06-24

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PRIOR APPLICATION NUMBER: 60/09069

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PRIOR APPLICATION NUMBER: 60/09069

PRIOR APPLICATION NUMBER: 60/09069

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PRIOR APPLICATION NUMBER: 60/09186

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Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
                              APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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Best Local Similarity 50.09
Matches 65; Conservative
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US-09-991-181-208
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
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                                                                           APPLICATION NUMBER: 60/088217
                                                                                                                                                                                  APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089599
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PPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090431
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75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
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PRIOR APPLICATION NUMBER: 60/090449
PRIOR FILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088617
PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-16
PRIOR PLILING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06-17
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PRIOR PRILING DATE: 1998-06-12
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC11
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CURRENT PELLING DATE: 2002-11-14
PRIOR PELLING DATE: 1997-01-17
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PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
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PRIOR PELLING DATE: 1998-02-26
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PRIOR PELLING DATE: 1998-05-07
PRIOR PELLORTION NUMBER: 60/08709
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PRIOR PELLING DATE: 1998-06-02
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Grimaldi, J. Christopher
Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                     Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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               Botstein, David
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                                          Desnoyers, Luc
                                                                                                                                Fond, Sherman
                                                                      Saton, Dan L
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APPLICANI: Zhango, Zemin

ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT PAPLICATION NUMBER: US/09/989, 734
CURRENT FILING DATE: 12001-11-19
PRIOR PELIOR TELING DATE: 1207-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
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PRIOR PELING DATE: 1998-0-25
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-0-0
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PRIOR PERIOR PELING DATE: 1
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Baker,Kevin P.
Botstein,David
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                                                                        Desnoyers, Luc
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                                                                               PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-24
PRIOR PELING DATE: 1938-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PELING DATE: 1938-06-26
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PELING DATE: 1938-06-26
PRIOR APPLICATION NUMBER: 60/091860
PRIOR PELING DATE: 1938-06-26
PRIOR APPLICATION NUMBER: 60/091860
PRIOR PELING DATE: 1938-07-01
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091638
PRIOR PELING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1938-07-07
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1938-07-07
PRIOR PELING DATE: 1938-07-07
PRIOR APPLICATION NUMBER: 60/091938
                      APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
PAPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09
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Matches 65; Conservative
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FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028

APPLICATION NUMBER: 60/088029 APPLICATION NUMBER: 60/088030 APPLICATION NUMBER: 60/088033

1998-06-04 1998-06-04 1998-06-04

1998-06-04

FILING DATE: LING DATE: LING DATE: LING DATE: FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167

US-09-989-734-208
Sequence 208, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

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R APPLICATION NUMBER: 60/088217
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R FILING DATE: 1998-06-09
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R APPLICATION NUMBER: 60/088738
R APPLICATION NUMBER: 60/088738
R APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 ILING DATE: 1998-06-17 PPLICATION NUMBER: 60/089598 ILING DATE: 1998-06-17 PPLICATION NUMBER: 60/089600 ILING DATE: 1998-06-17 PLICATION NUMBER: 60/089907 LING DATE: 1998-06-18 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 PAPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 PPLICATION NUMBER: 60/089532 ILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089538 PPLICATION NUMBER: 60/089599 LICATION NUMBER: 60/089653 FILING DATE: 1998-06-19 LING DATE: 1998-06-17 LING DATE: 1998-06-18 ILING DATE: 1998-06-22 ILING DATE: 1998-06-22 FILING DATE: 1998-06-22 ILING DATE: 1998-06-23 ILING DATE: 1998-06-23 LING DATE: 1998-06-16 LING DATE: 1998-06-17 ILING DATE: 1998-06-1 LING DATE: 1998-06-13 ING DATE: 1998-06-1 PRIOR PRIOR

135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194 649 TATGAGGITCTTACATTTTTTTTAGGCCAAGAGGCTGAAAAGGAAGAAAATGTTG 708 75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134 .; 0 ch 12.6%; Score 26; DB 9; Length 2095; 1 Similarity 50.0%; Pred. No. 39; 65; Conservative 0; Mismatches 65; Indels RESULT 56
US-09-997-653-208
US-09-997-653-208
Sequence 208, Application US/09997653
Publication No. US2030008297A1
GENERAL INFORMATION: R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-24 FILING DATE: 1998-06-25 1998-07-02 1998-07-02 FILING DATE: 1998-07-02 FILING DATE: 1998-06-24 FILING DATE: 1998-07-01 FILING DATE: 1998-06-2 195 TTATTATCCT 204 709 GCATTGTCCT 718 Best Local Similarity Matches 65; Conserv FILING DATE: FILING DATE: Query Match PRIOR
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FILING DATE:
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APPLICANT: Shang, Zening and I.

TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: 60/04290

PRIOR APPLICATION NUMBER: 60/04250

PRIOR PELING DATE: 1997-10-17

PRIOR PAPLICATION NUMBER: 60/065311

PRIOR PELING DATE: 1997-11-13

PRIOR PELING DATE: 1998-0-22

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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088326
R FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                              Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Ashkenazi, Avi J
                          Baker, Kevin P.
Botstein, David
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                                                                                   Desnoyers, Luc
                                                                                                                                                                    Fong, Sherman
                                                                                                              Eaton, Dan L.
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-09
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PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/090246
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-23
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PRIOR PELICATION NUMBER: 60/089598
PRIOR FILING DATE: 1938-06-17
PRIOR PELING DATE: 1938-06-17
PRIOR PLING DATE: 1938-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR PILING DATE: 1938-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1938-06-17
PRIOR PILING DATE: 1938-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
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APPLICATION UNMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089907
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.6%; Score 26; DB 9; Length 2095; Best Local Similarity 50.0%; Pred. No. 39; Matches 65; Conservative 0; Mismatches 65; Indels
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 161, Application US/10176758 ; Publication No. US20030008353A1
                                                                                                                                                                                                                                                      Watanabe, Colin K.
Wood, William I.
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                         Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P3430R1C42
                       APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                 Zhang, Zemin
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                 Pan, James
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GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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Pred. No. 39;
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              PRIOR APPLICATION NUMBER: 60/090435
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-
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Publication No. US20030008352A1
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Best Local Similarity 50.0%;
FILING DATE: 1998-06-24
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CURRENT APPLICATION NUMBER: US/09/993,667 CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065181
PRIOR APPLICATION NUMBER: 60/065311
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                65; Conservative
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Botstein, David
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                                                                                                                                                                                SEQ ID NO 161
                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Granaldi, Christopher J.
APPLICANT: Guraney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                        75 GATAATAGAACTAAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
                                                                             589 GATGTGAAAGCCAGGCCATTAGAGTTACTTGGGGTGAAAAAAAGTCTTGGTGGGGA 648
                                                                                                                     135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194
                                                                                                                                                           649 TATGAGGITCTTACATITITCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTG 708
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  0; Gaps
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  65; Indels
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  0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
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Publication No. US20030013855A1
GENERAL INFORMATION:
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Goddard, Audrey
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Smith, Victoria
Watanabe, Colin K.
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APPLICANT: Filvaroff, Ellen
  Conservative
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Goddard, Audrey
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Best Local Similarity
Matches 65; Conserv
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LENGTH: 2095
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US-10-063-616-35
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RICSO
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT APPLICATION NUMBER: US/10/175,737
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC4
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R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-66-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10 R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086028

R RFILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086029

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086030

R APPLICATION NUMBER: 60/086030

R APPLICATION NUMBER: 60/086031 APPLICATION NUMBER: 60/088824
FFILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 APLICATION NUMBER: 60/088326 TILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 TILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088810 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/066770 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/087106 LLING DATE: 1998-06-10 ING DATE: 1998-06-05 1998-04-28 FILING DATE: 1997-11-13 FILING DATE: 1998-05-07 1998-06-1 LING DATE: PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/08960
PRIOR PLILING DATE: 1998-06-19
PRIOR PRILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-19
PRIOR PRILING DATE: 1998-06-22
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PRIOR PRILING DATE: 1998-06-23
PRIOR PRILING DATE: 1998-06-24
PRIOR PRILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-26
PRIOR PRILING DATE: 1998-06-26
PRIOR PRILING DATE: 199

FILING DATE: 1998-07-02

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
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PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
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PRIOR PELING DATE: 1998-07-07
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood will:--
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Publication No. US20030023042A1
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Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 50.08
Marches 65; Conservative
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ORGANISM: Homo Sapien
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Best Local Similarity
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/10/175,738
PYIOR TPLING DATE: 2002-06-19
PYIOR APPLICATION CONSISTED TO SEE FILE WRAPPER OF PAIM
NUMBER OF SEQ ID NOS: 612
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CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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; Publication No. US20030022293A1
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Wood, William I.
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 50.0%
Matches 65; Conservative
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Gurney, Austin L.
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Smith, Victoria
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Goddard, Audrey
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709 GCATTGTCCT 718
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                                                                                     RESULT 63
US-10-173-706-161
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Best Local Similarity
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: 105/10/175,752
CURRENT FILING DATE: 2002-06-19
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                                                                                                                                    65; Indels
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                                                                                                   Score 26;
Pred. No.
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; Publication No. US20030022296A1
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Publication No. US20030022295A1
GENERAL INFORMATION:
                                                                                                   12.6%;
50.0%;
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
                                                                                               Query Match
Best Local Similarity 50.0%
Matches 65, Conservative
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Smith, Victoria
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CORGANISM: Homo Sapien
US-10-175-752-161
                              TYPE: DNA
ORGANISM: Homo Sapien
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Best Local Similarity
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US-10-175-752-161
                                                                 US-10-175-738-161
                 LENGTH: 2095
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 SEQ ID NO 161
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C86
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches
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50.0%;
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
                                                                 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                     Pan, James
Smith, Victoria
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APPLICANT: Baker, Kevin P.
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US-10-176-757-161
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US-10-176-757-161
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FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 161, Application US/10180557; Publication No. US20030022301A1; GENERAL INFORMATION:
                  Watanabe, Colin K.
Wood, William I.
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                  65; Conservative
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US-10-180-552-161
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Best Local Similarity
Matches 65; Conserv
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LENGTH: 209
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Best Local
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                              75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
                                                               TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194
                                                                                                                                649 TATGAGGITCTTACATITITCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTG 708
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 65; Indels
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 0; Mismatches
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Publication No. US20030022300A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                           Sequence 161, Application US/10176913
Publication No. US20030022298A1
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 50.0%
 Conservative
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ORGANISM: Homo Sapien
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P34.50RLC153
CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT APPLICATION NUMBER: US/10/180,552
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 161
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PRIOR APPLICATION NUMBER: 60/08026
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
PRIOR APPLICATION NUMBER: 60/08030
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-07
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PRIOR FILING DATE: 1998-06-05
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PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C3
CURRENT APPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2001-11-14
              649 TATGAGGTTCTTACATTTTTTTTTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-24
PRIOR PLING DATE: 1997-11-24
PRIOR PLING DATE: 1998-02-25
PRIOR PLING DATE: 1998-04-26
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-07
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-07
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Sequence 208, Application US/09990438
Publication No. US20030027754A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Goddard, Audrey
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Kljavin, Ivar J.
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Botstein, David
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Tumas, Daniel
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649 TATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708
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                                                                                                   PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090359
PRIOR APPLICATION NUMBER: 60/090359
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-02
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091982
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Matches 65, Conservative
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APPLICANT: Wood, william 1.

APPLICANT: Zhang, Zemin
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITTLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT SPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-11-12
PRIOR PLILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-01-124
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
Sequence 208, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/087609
PRIOR PILING DATE: 1998-06-07
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088021
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Kljavin, Ivar J.
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Eaton, Dan L.
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APPLICATION NUMBER: 60/088025

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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-10 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 LING DATE: 1998-06-10 PPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 PPLICATION NUMBER: 60/089105 [LING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/08810 APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 PLICATION NUMBER: 60/088734 ILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 PPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-18 FILING DATE: 1998-06-18 1998-06-04 1998-06-04 FILING DATE: 1998-06-05 LING DATE: 1998-06-16 ILING DATE: 1998-06-17 1998-06-04 LING DATE: 1998-06-1 PRIOR

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PRIOR APPLICATION NUMBER: 60/090246

PRIOR APPLICATION NUMBER: 60/090252

PRIOR APPLICATION NUMBER: 60/090252

PRIOR APPLICATION NUMBER: 60/090254

PRIOR APPLICATION NUMBER: 60/090355

PRIOR APPLICATION NUMBER: 60/090355

PRIOR APPLICATION NUMBER: 60/09035

PRIOR APPLICATION NUMBER: 60/090355

PRIOR APPLICATION NUMBER: 60/09035

PRIOR APPLICATION NUMBER: 60/090415

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PRIOR APPLICATION NUMBER: 60/09045

PRIOR APPLICATION NUMBER: 60/09045

PRIOR APPLICATION NUMBER: 60/09054

PRIOR PLILING DATE: 1998-66-24

PRIOR PLILING DATE: 1998-66-24

PRIOR PLILING DATE: 1998-66-24

PRIOR PLILING DATE: 1998-66-25

PRIOR PPLILON NUMBER: 60/090665

PRIOR PLILING DATE: 1998-66-26

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Query Match 12.6%; Score 26; DB 9; Length 2095; Best Local Similarity 50.0%; Pred. No. 39; Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC44
FILE REFERENCE: P2730PLC44
CURRENT APPLICATION NUMBER: US/09/997, 428
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
649 TATGAGGTICTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAAGACAAAATGTTG 708
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PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/0730
PRIOR PELING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR PILING DATE: 1998-04-28
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-06-02
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Publication No. US20030027162A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 66/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 66/088021
FILING DATE: 1998-06-04
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Paoni, Nicholas F.
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PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1938-06-04
PRIOR PELICATION NUMBER: 60/088026
PRIOR PELICATION NUMBER: 60/088028
PRIOR PILING DATE: 1938-06-04
PRIOR PILING DATE: 1938-06-05
PRIOR PILING DATE: 1938-06-10
PRIOR PILING DATE: 1938-06-17
PRIOR PILING DATE: 1938-06-17
PRIOR PILING DATE: 1938-06-17
PRIOR PILING DATE: 1938-06-17
PRIOR PILING DATE: 1938-06-18
PRIOR PILING DATE: 1
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C42
                   135 TAACAGGICCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIG 194
                                                                     649 rargaggircriacaritrircriatraggccaagaggcigaaaaggaagacaaaatgirg 708
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CURRENT FILING DATE: 2001-11-15
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062260
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1999-11-24
PRIOR PELING DATE: 1999-10-25
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-07
                                                                                                                                                                                                                                                                                                         Sequence 208, Application US/09997666 Publication No. US20030027163A1 GENERAL INFORMATION:
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Gurney, Austin L.
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Stewart, Timothy A.
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Goddard, Audrey
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Botstein, David
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US-09-997-666-208
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Pred. No. 39;
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PRIOR APPLICATION NUMBER: 60/090252
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
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PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PELING DATE: 1998-07-07
PRIOR 
                      APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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12.6%;
Best Local Similarity 50.0%;
Matches 65; Conservative
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088021

589 GATGTGAAAGCCAGGCCATTAGAGTTACTTGGGGTGAAAAAAAGTCTTGGTGGGA 648

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FILING DATE: 1998-06-03

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R APPLICATION NUMBER: 60/088202
R APLIJON DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
                      R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
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R APPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04
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R PAPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088326
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION UNDBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/088876
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
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FILING DATE: 1998-06-18
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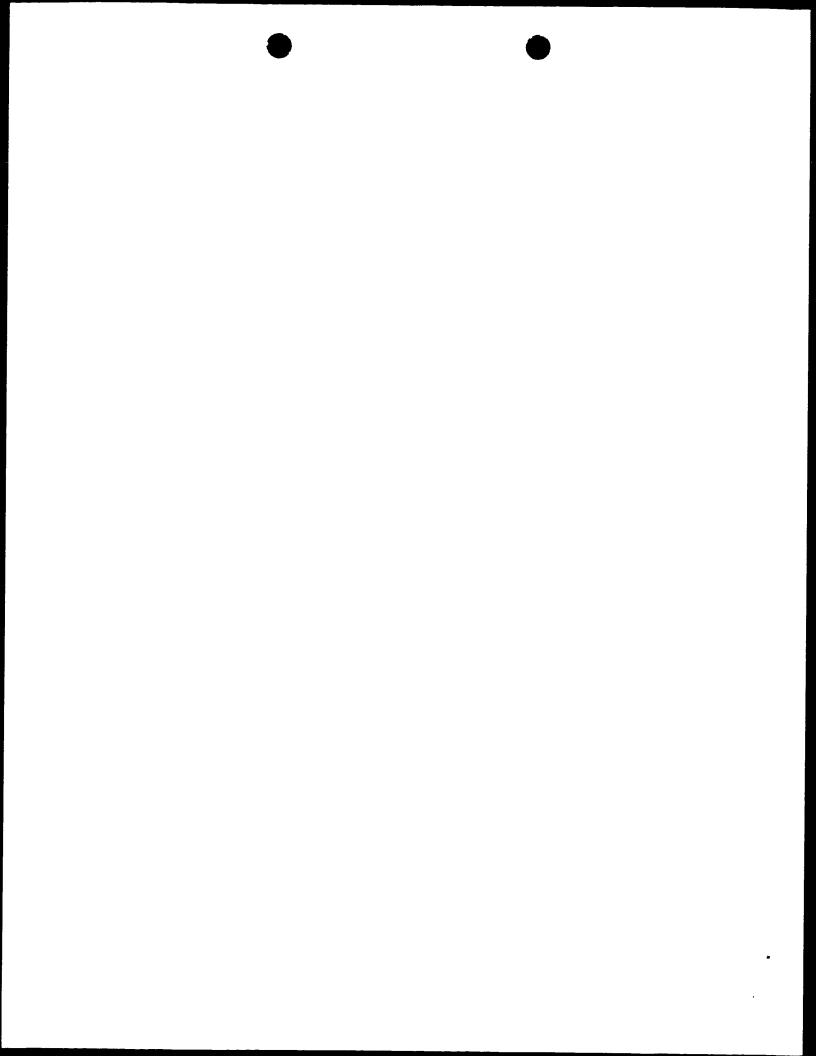
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PRIOR PAPLICATION NUMBER: 60/08952
PRIOR FILING DATE: 1998 6612
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PRIOR PAPLICATION NUMBER: 60/09035
PRIOR PAPLICATION NUMBER: 60/09035
PRIOR PLILING DATE: 1998 6624
PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09043
PRIOR PLILING DATE: 1998 6624
PRIOR APPLICATION NUMBER: 60/09045
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PRIOR APPLICATION NUMBER: 60/09045
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PRIOR PRILING DATE: 1998 6626
PRIOR PRILING DATE: 1998 60701
PRIOR PRILING DATE
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Query Match
12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; G

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 TATGAGGTTCTTATTTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTG 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TAACAGGICCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGGAGGIG 194
                                                                    589 gargrgaaagccaggccagrcarragagrractrgggggaaaaaaaagrcrrgggggga 648
589 GATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAAGTCTTGGTGGGGA 648
                                           135 TAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTG 194
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US-10-13-700-161
Sequence 161, Application US/10173700
Publication No. US20030027262A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo Sapien
US-10-173-700-161
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LENGTH: 2095
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Human neuregulin-1

Nucleotide sequenc Human ABC1 genomic Human prostate exp Human gene express Maize dwarf mosaic

Human ovarian anti

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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AAV17601
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AAC45029
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AAC01804
AAZ33507
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AAZ89157
AAZ90999
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AAF94886
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ABL48836
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ABL54334
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| SIDS2/ggddata/geneseqn_embl/NA1999.DAT:
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| SIDS2/gcgdata/geneseqn/geneseqn_embl/NA2000.DAT:
| SIDS2/gcgdata/geneseqn/geneseqn_embl/NA2001A.DAT:
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| SIDS2/gcgdata/geneseqn/geneseqn_embl/NA2001B.DAT:
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Drosophila melanog Human Oestrogen re Arabidopsis thalia Cat flea hindgut a

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Result No.

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99US-0134218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  982 TCGAGATCAAAACTAATCCACTAAGCTTCAAGACTTAAACTTACATCTGTTGGCAACCAAT 923
                                                                                                                                                                                                                                                                                                                                                                                                            1042 GACTCATTATATGATCACATATAAAACAAAGGCGTGAGCCGCATCACATAGCCTATGGT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
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Lafleur DW;
Shi Y, Soppet DR;
                                                                                                                                                                                                                                           18.3%; Score 37.6; DB 21; Length 1622; llarity 53.4%; Pred. No. 0.016; Conservative 0; Mismatches 69; Indels 0;
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, Florence KA, Komatsoulis GA,
Olsen HS, Rosen CA, Ruben SM,
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                   990S-0161359
990S-0161360.
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P-PSDB; AAY07803.
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                      26-OCT-1999;
26-OCT-1999;
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79; C
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Moore PA,
Young PE;
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P-PSDB; AAB87746.

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the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in AAV37369-X37441.
                                                                                                                                 This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, rat, mouse, T2R; taste receptor; G-protein coupled receptor; taste transduction G-protein coupled receptor; identification; tongue; taste sensory neuron; taste cell; taste modulator; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 ACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATA 78
                New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 32.6; DB 20; Length 831; 57.3%; Pred. No. 0.61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 831 BP; 273 A; 125 C; 163 G; 267 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 ATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 Grgcaggaaamcaagaagaararrrrrcagagraragrcaaaa 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                Claim 1a; Page 224; 280pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF92516 standard; DNA; 876 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taste signalling pathway; ds
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Matches 59; Conserv
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WPI; 2001-211396/21

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AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB8731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for
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                             Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be used in food and pharmaceutical industries to customize taste, for e.g. to decrease the bitter taste of food
                                                                                                                                                                                                                                                                                                                                                           pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in food and pharmaceutical industries to customise taste, for e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 gaccagieciaiganenieiarcreciregreagreateceareaeadaaadaigeigeage 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 14005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.2; DB 22; Length 876; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 876 BP; 215 A; 205 C; 163 G; 293 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    decrease the bitter taste of food or drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                              Disclosure; Page 173-174; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers
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11-JUL-2000; 2000US-0614150.
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hes 60; Conservative
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                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome 6q.25.1; single nucleotide polymorphism; cardiovascular disease; autoimmune disease; systemic lupus erythematosus; arthriis; rheumatism; osteoparosis; breast cancer; endometrial cancer.
                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7655 Tróradricicegiadrifaceresectracarificeseserececasecessations 7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7715 ACGAATCGGACAACTCAATGGTTGGTCGTGTCCCCAGGATTCGTTGATTTGAATAGCC 7774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oestrogen receptor gene and protein polymorphisms useful for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 ACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACATCCTGTGACTAACAGGTC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 TACGAGITCTIGGICAATITCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 30.8; DB 23; Length 15165; 48.8%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7775 GACATTAGCACACATTTCCTGCGACTCAAAGTCAAACAAGCCATGT 7824
Claim 1; SEQ ID NO 14005; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15165 BP; 4093 A; 3274 C; 3399 G; 4399 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of individuals at risk of developing bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hwang SS, Winn-Deen ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Oestrogen receptor beta gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS43104 standard; DNA; 325791 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.8%;
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24-JAN-2001; 2001US-0768185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalush F, Cassel MJ,
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10 amino acids), antibodies galing them, nucleic acids encoding them (including vectors for transforming cells). The gene for human Embera is located on chromosome 6q.25.1. The variants are encoded by single nucleotide polymorphisms (SNP). The variant pepildes and proteins can be used in assays to determine the biological activity of the protein, to raise antibodies, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, to identify compounds that modulate receptor activity and to screen compounds for the ability to stimulate or inhibit interaction between the receptor protein and a target molecule that normally interacts with the receptor protein e.g. cetrogen. The antibody can be used to isolate the protein, to assess expression in
                                                                                                                                                                                                                                                                                                                                                                                          disease states e.g. cardiovascular disease and autoimmune disease (e.g. systemic lupus erythematosus, arthritis, rheumatism and osteoarthritis), osteoporosis, breast cancer and endometrial cancer. In addition
of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 90917 TGGAGGCATGGTATGGAGGTAAATGGGTCCTTGGCCTCTCTCCTGGATTCAAGTCCTTC 90975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the binding of the oestrogen receptor protein to a binding partner such as a ligand. The nucleic acids encoding the proteins can be used as probes, primers, chemical intermediates and in biological assays. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 325791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 30.2; DB 69.5%; Pred. No. 35; cive 0; Mismatches
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Les 41; Conservative
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LEDFORD B L.
WOESSNER J P.
HAAS W D.
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HAMILTON C M.
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RAINES T M.
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SLATER T.
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ALLEN K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human ERbeta gene.
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(SLAT/)
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                                                                                                                                                                                                                                                                                   The invention relates to a novel nucleic acid of Arabidopsis thaliana comprising a sequence capable of hybridising under stringency to one of the 999 sequences referred to but not defined in the specification (ABOSB131-ABOSB129). The nucleic acid sequences are useful to identify homologous or related genes, to produce compositions that modulate expression or function of the encoded protein, to map functional regions of the protein, to study associated physiological pathways, to genetically manipulate cells and plants. The encoded products are useful to screen for biologically active agents such as fungicides or
                                                                                                                                                          New nucleic acid sequences of Arabidopsis thaliana and their encoded products are useful to produce transgenic plants, to screen for biologically active agents such as fungicides and insecticides and in genetic studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACATCCTGTGAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 GATTATTGACGGTAGGACCAATGGCTGCGATGGCTGGATCGAGAGCGAATGACTGATGAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 AAGGAGGGTTATGATTACTGGGTCGATGACCGTTAGATTGCCAATTCGACGGAGAAAG 203
                                                                 Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                              Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas W
', Davis KR, Allen K, Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 ATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 24; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flea infestation; vaccine; antiparasitic; therapeutic target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 917; 18pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides and to elucidate biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 335 BP; 66 A; 115 C; 51 G; 99 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 29.6; Di
ilarity 51.5%; Pred. No. 4.6;
Conservative 0; Mismatches
                                                               Mathew AV, ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC93962 standard; cDNA; 498 BP
                                               An Y, Hamilton CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0128704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000WO-US09437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; detection; ss.
                                                                 Page A, M
Kricker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ctenocephalides felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 TAACAGGTCCAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GCTGAGGACCTT 131
                                                                                                                                   WPI; 2002-479265/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP.
(HOFF/) HOFFMAN N.
                 (HURB/) HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200061621-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2000.
                                              Gorlach J,
Rameaka JG,
                                                                               Garcia CA,
Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC93962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, and compositions comprising the inhibitors of the proteins, and compositions comprising the inhibitors of administration to an animal. The nucleic acids, and the proteins they concome may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid cand quantitate the presence of cat flea or other homologous nucleic acid controlled in mamples. They may also be used to study the expression and cfunction of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific cantibodies, and in assays to identify modulacros (aponists may also be used to anti-HMT/HNC protein antibodies and antagonists may also be used to downrequiate protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to envire the presence of downrequiate protein expression and activity. The nead as antigens and antagonists may also be used to envirant the presence of downrequiate protein expression and activity. The nead as antigens and antagonists may also be used to envirant the presence of float the presence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                     Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea infestations -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498 AATGTAGCTCAAACTGATAATGCTCACCATGAACAGAATTATGGANCTTTNATATNGGAN 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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     Wisnewski N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 498 BP; 164 A; 84 C; 88 G; 153 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HPCQ091 cDNA, SEQ ID NO:1794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 ACACTGATGTTTINACGGCTTCAAATCTGGTGTGAAT 402
     Stinchcomb DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Page 397; 964pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ55914 standard; cDNA; 603
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Gaines PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                 WPI; 2000-656323/63.
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     Brandt KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ55914;
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Homo sapiens.

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C RBP4122B) and to CNAS encoding them (ABD54111-ABD565B), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against thuman ovarian antigens and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, creenting, prognosing or preventing vary and/or breast related disorders. Such conditions include ovarian antigens, and the use of ovarian or preventing vary and/or breast related disorders (e.g., infertility, disorders of pregnancy, anovalation, polycystic ovary syndrome, ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system constructs infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastifis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies autoimmune oophoritis, systemic lupus erythematosus), confortator disorders (e.g., aneamia), cardiovascular disorders, respiratory disorders. Ovarian antigen polypeptides and urinary system disorders. Ovarian antigen polypeptides and modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the condition of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies condition of individuals and in forensic analysis, and the polymeral in disease diagnosis, drug targeting and phenotroning mentions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 AGGIATAAATATCGAGTAGCTTTTAAACAAACCACCTGACCAAGAAGGGAANTGAGCTTG 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                             07-JUN-2000; 2000US-209467P.
                                                                                                                                                                     07-JUN-2001; 2001WO-US18569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABP42837.
WO200200677-A1.
                                                                                  03-JAN-2002.
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protein (APP). The invention relates to a protease, e'g human aspartyl protease 2 (Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or DTG separated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New enzyme designated human aspartase useful in research into
Alzheimer's Disease is capable of cleaving amyloid protein precursor at
the beta secretase site to produce amyloid beta peptide
                                                                                                                   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is used in the modification of human amyloid precursor
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"Represented in the specification as 0"
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/note= "Represented in the specification as 0"
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                                                                                                                                                                                                                                                                                                                                                                                                "Represented in the specification as
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"Represented in the specification as
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"Represented in the specification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parodi LA,
                                                                                                                               Alzheimer's disease; beta secretase site; ss.
                                                                                           Nucleotide sequence used in APP modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinrikson RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 182; 183pp; English.
                                                                                                                                                                             Location/Qualifiers
           :691/c
AAA15691 standard; DNA; 462 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US20881.
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                                                                   03-AUG-2000 (first entry)
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/note= '
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                                                                                                                                                                                         misc feature
                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                      Synthetic.
                                             AAA15691;
RESULT 11
           AAA15691/
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100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal trighyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 KYNRYTKKSANKGHHYWVTAMMDRYANAYNTGNTNNTHGNVNNTHCHAAGTTCTTTGAGA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AATTICCAGGACACAGAIGAITICGGICCAAGAACAGGAIAAIAGAACIAAGCAACGCGAI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%; Score 29.2; DB 21; Length 462; 22.5%; Pred. No. 7; ative 46; Mismatches 47; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clee SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 462 BP; 96 A; 76 C; 33 G; 88 T; 169 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayden MR, Brooks-Wilson AR, Pimstone SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 1; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF92831 standard; DNA; 183999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1999; 99US-0151977.
15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ABC1 genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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    (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient,
    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;

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                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                    127 CCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAA 186
                                                                                                                                                  67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) compris a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                  Gaps
                                                 Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                   Length 183999;
                                                                                                                  .
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lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                  Indels
                                                                                 DB 22;
                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 51274.
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                   62;
                                                                               Score 29.2;
Pred. No. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 9967; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monahan JE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                         13483 GTAAAGTGGTGTGCACCT 13500
                                                                                 14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                            ABV51283 standard; cDNA; 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-UUN-2000; 2000US-211314P.
18-UUL-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US05171.
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                                                                                                                                                                                                                                                                                       187 GCAAGGTGTTATTATCCT 204
                                                               Ouery Match
Best Local Similarity bureary 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2
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ABV51283/
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determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                          46 AGGACACAGATGGTTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                   (1) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                      14.1%; Score 29; DB 23; Length 526; 54.1%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene expression product cDNA sequence SEQ ID NO:3551.
                                                                                                                                                                                                                                                             106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTC 154
                                                                                                                                                                                                                                                                                   320 AGACGAATGGAAGACTACATTCTTCTACTGACTGGTCATCGGTTTTTC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                         50; Indels
                                                                                   Sequence 526 BP; 164 A; 95 C; 74 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1695; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    AAZ16081 standard; cDNA; 765 BP
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98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999 (first entry)
                                                                                                                                                       59; Conservative
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Escobedo J, Gaic...
WL, Kassam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-494092/41.
                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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31-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ16081;
                                                                                                                      Query Match
                                                                                                                                                         Matches
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(g)
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mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polymucleotides can be used for raising antibodises for experimental, diagnostic and therapeutic purposes. The polymucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polymucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polymucleotides can also be used to screen for
                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                    31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGC 90
                                                                                                                                                                                                                                                                                                                                17 rcrrccrnrrrgcaggarcccarccarccaragagaragargcgrcagggaaagc 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDMV-B; viral resistance; disease resistance; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monocot; P3 proteinase; NIa proteinase; NIb replicase;
RNA-dependent RNA polymerase; coat protein; Zea mays; sorghum;
sugarcane; Saccharum officinale; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= a
'product= polyprotein encoded by MDMV-B genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product = 3-prime sequence of helper component
                                                                                                                                                                                                                                       14.1%; Score 29; DB 20; Length 765;
                                                                                                                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= cylindrical inclusion protein
                                                                                                                                                                                                         Seguence 765 BP; 204 A; 145 C; 186 G; 227 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                               91 AACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTG 132
                                                                                                                                                                                                                                                                                                                                                                                              77 CAAGATGGAAATGGATGGGAATGAATGAGGAACATGATGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteinase (HC-Pro)
                                                                                                                                                                                                                                                     Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= K2 (6 kDa protein)
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= g
product= NIa proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= P3 proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= NIb replicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize dwarf mosaic virus genomic RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                         peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize dwarf mosaic virus strain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT47073 standard; RNA; 8543
                                                                                                                                                                                                                                                     54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5745..7307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2376..4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293..4451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7308..8291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Φ
                                                                                                                                                                                                                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8291
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                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L5-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT47073;
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                      datches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1679 TCTGAACACACGCCATATTGCTGAAATTTTTCCACAGTATGACAATTCTGCCCATGATTG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACA 73
                                                                                                                                                                                                                                                                                                                                         The sequence of the polycistronic messenger RNA of maize dwarf mosaic virus strain B (MDMV-B) is given in AAT47073 and the encoded MDMV-B polyprotein in AAW10344. New chimaeric genes (see also AAAT47074) comprise a mnoococyledonous plant promoter linked to a modified nucleic acid sequence derived from the MDMV-B genome. The modification is such that mRNA is translated to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the translation initiation codon or includes a premature srop codon. Expression of the chimaeric gene inhibits infection of plants (pref. sorghum, sugarcane, esp. maize) by MDMV. The transgenic plants display an inheritable resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
                                                                                                                                                                                                                                                    contains
                                                                                                                                                                                                                                               Chimaeric gene for imparting viral resistance to plants - conta: sequence modified to express non-translatable mRNA, or non-coat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8543 BP; 2913 A; 1637 C; 1820 G; 2160 U; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                               Disclosure; Page 31-44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK95240 standard; DNA; 1503900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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52.0%;
                                                                           96WO-EP02673
                                                                                                        95US-0496944
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                                                                                                                                       (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                   WPI; 1997-108965/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                      Dietz JM, Law MD;
                                                                                                                                                                                                                P-PSDB; AAW10344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1559 ATACC 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164876-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 CTAAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                  viral protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                         20-JUN-1996;
                                                                                                        30-JUN-1995;
              WO9702352-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                            23 - JAN - 1997
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NEGLAGIO of the invention. The NEGLAGI gene is also referred to as the human Schizophrenia gene. The invention also relates to fragments or variants of the gene and the NEGLAGI polypeptides they encode. The NEGLAGI nucleic acids and polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NRGLAGI expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of NRGLAGI by expressing inactive proteins or to supplement the patients own production of NRGLAGI. Additionally, the gene may be used to produce NRGLAGI polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene may also be used as culturing the cell to express the protein. The gene may also be used as DNA probes and primers in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The NRGLAGI polypeptides may also be used as antigens in the production of antibodies against NRGLAGI antibodies and antagonists may also be used to activity. Anti-NRGLAGI antibodies and antagonists may also be used to activity. Anti-NRGLAGI antibodies and antagonists may also be used to activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           down regulate expression and activity. Anti-NRG1AG1 antibodies may also be used as diagnostic agents for detecting the presence of NRG1AG1 polypeptides in samples. NRG1AG1 is associated with schizophrenia which may be prevented, diagnosed and/or treated by the above methods.
                                                                                                                                                                                                                                                                                                                                                                                                           Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for preventing diagnosing and treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                                                                                                       WPI; 2001-550179/61.
P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905, AAG67909, AAG67909, AAG67910, AAG67911, AAG67912, AAG67906, AAG67907, AAG67908, AAG67909, AAG67917, AAG67918, AAG67919, AAG67913, AAG67913, AAG67913, AAG67913, AAG67913, AAG67913, AAG67913, AAG67914, AAG67915, AAG67913, AAG67914, AAG67915, AAG67918, AAG67926,
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                                                                                                                                                                                                                                                                                                                              AAG67933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human neuregulin-1 associated gene 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 22; Length 1503900;
Pred. No. 1.5e+02;
0; Mismatches 50; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 504809 AGACGAAIGGAAGACIACAIICIIICIACIGACIGGICAICGGIIIIIC 504857
                                                                                                                                                                                                                                                                                                   AAGG7920, AAGG7921, AAGG7922, AAGG7923, AAGG7924, AAGG7925,
AAGG7927, AAGG7928, AAGG7929, AAGG7930, AAGG7931, AAGG7932,
AAGG7934, AAGG7935, AAGG7936, AAGG7937.
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                                                                                                                                                       Steinthorsdottir V, Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 90-501; 750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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28-FEB-2001; 2001WO-US06376.
                                                     28-FEB-2000; 2000US-0515715
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Matches 59; Conservative
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                                                                                                       (DECO-) DECODE GENETICS
                                                                                                                                                       Stefansson H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-2001
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The invention also relates to fragments or variants of the neurequin.

Gene. The gene and its proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate neuregulin. I expression, such as schizophrenia. For example they may be used to treat disorders associated with decreased neuregulin 1 expression by rectifying mutations or deletions in a patient's genome that affect the activity of neuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the mucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar culturing the cell cacids in samples, and therefore which patients may be in need of restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antibodies may also be used to down regulate expression and activity. The antibodies and mattagonists may also be used as diagnostic agents for detecting the presence of neuregulin 1 in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human neuregulin 1 gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                                                                                                                                                                                                                            P-PGDB; AAGG7948, AAGG7939, AAGG7940, AAGG7941, AAGG7942, AAGG7943, AAGG7944, AAGG7945, AAGG7946, AAGG7947, AAGG7948, AAGG7949, AAGG7950, AAGG7951, AAGG7952, AAGG7953, AAGG7954, AAGG7955, AAGG7958, AAGG7958, AAGG7959, AAGG7956, AAGG7957, AAGG7958, AAGG7959, AAGG7960, AAGG7961, AAGG7962, AAGG7962, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7967, AAGG796796, AAGG7967, AAGG796796, AAGG796796, AAGG796796, AAGG796796, AAGG7967969, AAGG796796, AAGG7971, AAGG7971, AAGG7971, AAGG7971,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuregulin 1 nucleic acids and proteins useful for diagnosing preventing and treating schizophrenia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 504809 AGACGAATGGAAGACTACATTCTTACTGACTGGTCATCGGTTTTTC 504857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%; Score 29; DB 22; 54.1%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                  Steinthorsdottir V, Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                    28-FEB-2001; 2001WO-US06377.
                                                                                                                                                                 28-FEB-2000; 2000US-0515716
                                                                                                                                                                                                                 (DECO-) DECODE GENETICS EHF
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Matches 59; Conservative
                                                                                                                                                                                                                                                                                                               WPI; 2001-514841/56.
                      WO200164877-A2.
                                                                                                                                                                                                                                                                  Stefansson H,
                                                                    07-SEP-2001.
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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
       expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae, Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                  Olsen PB;
                                                                                                                                                                                                 Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG,
Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                               substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                  Claim 86; Page 1672; 3161pp; English.
                                                                                                                                                                  (NOVO ) NOVO NORDISK BIOTECH INC.
                                                                                                                          22-MAR-2000; 2000WO-US07781.
                                                                                                                                               99US-0273623.
                                                                                                                                                                              (NOVO ) NOVO NORDISK AS
                                                                                                                                                                                                                      WPI; 2000-594572/56
                                                             Fusarium venenatum.
                                                                                 WO200056762-A2.
                                                                                                                                               22-MAR-1999;
                                                                                                     28-SEP-2000
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The FF cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be identified and gene copy number variation and stability can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in outlure conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from all specifically claimed in the present invention.

. 0 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCT 129 139 ATCTTGTTTTTATGACGACNAATTGCATTGATATTTGGGGGGATTGGCAACTTGCTATAT 198 130 GIGACTAACAGGICCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCA 189 Gaps . 0 Match 14.0%; Score 28.8; DB 21; Length 300; Local Similarity 50.8%; Pred. No. 8.2; Indels 64; Sequence 300 BP; 86 A; 53 C; 65 G; 90 T; 6 other; 0; Mismatches Conservative 190 AGGTGTTATT 199 99 Query Match **fatches** 70 199 qq ò g ò

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0; Gaps

259 AGCTGTTCTT 268

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RESULT 19

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)

recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptoroccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule encoding a process comprising: (a) screening of a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the isolating the nucleic acid molecules from the members; or (b) isolating many which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome to prime systemsian modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2357 ACCAAAAGGATTGTTTGATAAGCTACTTTCTGTCTCTAACAATTCCCTAGCTTGATCCGA 2416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                            Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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Pred. No. 18;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dougherty BA, Fannon M;
                                                                                                                                       Streptococcus pneumoniae genome fragment SEQ ID NO:216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1220-1222; 1409pp; English
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                AAV52349 standard; DNA; 2651 BP
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Matches 45; Conservative (
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                                                                                             (first entry
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                                                                                                                                                                                                                                                                                                                                                           30-OCT-1997;
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AAV52349
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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Pred. No. 22;
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                                                                   ABL21466 standard; DNA; 4718 BP
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60.0%;
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11-JUL-2000; 2000US-0614150.
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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ID ABL3
RESULT 20
                                ABL21466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 19382 AAAGGAAAAGATGTTTCGTATACGCAATCGATTTGGATTTAGAGTGCCATAAAATTAACT 19323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 19442 AGCCATAGATCACCGATCTCTGGTTATTTATAGAGCTGCTGAAACGTCAGTG 19383
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                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 23732;
Drosophila melanogaster genomic polynucleotide SEQ ID NO 42379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer associated coding sequence SEQ ID NO: 77.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23732 BP; 6358 A; 4988 C; 5137 G; 7249 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 42379; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 28.8; DB
ilarity 52.5%; Pred. No. 40;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF94886 standard; cDNA; 396
                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                 pharmaceutical; gene; ds.
                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200118046-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions -
                                                                                                                                                              WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001.
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                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF94886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
X D X B X S X M X B X B X B X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X C S X 
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The present invention provides a number of coding sequences and proteins, the over-expression of which is associated with ovarian carcinoma/cancer. These can be used in the diagnosis, treatment and prevention of ovarian cancer, optionally by gene therapy or in the form of a vaccine. The present sequence is an example of one of these sequences.
                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptides associated with ovarian carcinomas, and the nucleic acids that encode them, useful for the prevention diagnosis and treatment of ovarian cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GTTAAATNCNGGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATGCATATA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 GTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian carcinoma associated coding sequence SEQ ID NO: 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 GATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ACTACTATACAGGNGATNTGCAAAACCCCTACTGGGAAATCCATTTCATTAGTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 28.6; DB 22; Length 396; 50.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molesh DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 140; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT03153 standard; cDNA; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stolk JA, Algate PA,
10-SEP-1999; 99US-0394374.
01-MAY-2000; 2000US-0561778.
15-AUG-2000; 2000US-0640173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2000; 2000US-0713550.
03-APR-2001; 2001US-0825294.
02-OCT-2001; 2001US-0970966.
                                                                                            07-SEP-2000; 2000US-0656668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.49
nes 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                      WPI; 2001-211395/21.
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                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                          Stolk JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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patient and for determining the presence of a cancer in a patient.
                                                                                                                                                                               0; Mismatches
                                                                                                                                                        Score 28.6;
                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast AFC1 gene encoding Afc1p protein.
                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rine JD;
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/transl_except=
                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame
                                                                                                                                                                                                                                                                                                                                         AAV17601 standard; DNA; 1825
                                                                                                                                                        13.9%;
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                                                                                                                                                                     50.4%;
                                                                                                          ovarian carcinoma proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VĽ,
                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342..1704
                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashby MN, Boyartchuk
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                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in
                                                       The present invention provides human ovarian cancer associated proteins and coding sequences. The sequences can be used in the diagnosis and treatment of ovarian cancers. The present sequence is a coding sequence
 pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                            Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
                                                                                                                                                                                                                    74 GTTAAATNCNGGGACNCCTTACAATTGTGTAAANAACATGCNCANAAACATATGCATATA 133
                                                                                                                                                                     0; Gaps
                                                                                                                                                                                             GTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer
                                                                                                                                                                                                                                            GATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTT 150
                                                                                                                                                                                                                                                                  134 ACTACTATACAGGNGAINTGCAAAACCCCTACTGGGAAATCCATTTCATTAGTT 188
                                                                                                                                             DB 24; Length 396;
                                                                                                                                                                    Indels
                                                                                                                     Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;
                                                                                                                                                                     57;
                                                                                                                                                         Pred. No. 11;
0; Mismatches
                                                                                                                                             13.9%; Score 28.6; 50.4%; Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                       Ovarian carcinoma sequence isolate 24679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fling SP
                                   Example 1; Page 139; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 64; 131pp; English.
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                                                                                                                                                                                                                                                                                                                              ABL48836 standard; cDNA; 396
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01-MAY-2000; 2000US-0561778.
15-AUG-2000; 2000US-0640173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0656668
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                                                                                                                                                        Local Similarity 50.4
tes 58; Conservative
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ALGATE P A.
FLING S P.
                                                                                               of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002004491-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (STOL/)
(ALGA/)
(FLIN/)
                                                                                                                                             Query Match
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                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                        RESULT 24
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The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The sequences given in records ABL489760-ABL48956 represent polynucleotides encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GITAAAINCNGGGACNCCITACAAITGIGTAAANAACAIGCNCANAAACAIATGCATATA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 GTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGC 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFC1 gene; Afc1p; a-factor convertase; CAAX protease; zinc metalloprotease; yeast; prenylation; Ras; inhibitor; cancer; colorectal carcinoma; pancreas carcinoma; leukaemia; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GATACAATTIGGGIGGATIGGCAACAACTICCTGIGACTAACAGGICCATAGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 ACTACTATACAGGNGATNTGCAAAAACCCCTACTGGGAAATCCATTTCATTAGTT 188
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/transl_except= (pos:702..705, aa:Ser)
/note= "this codon has an apparent 1 nuclectide
insertion, which alters the reading
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(pos:1663..1665, aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;
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04-MAY-1999,
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                                                                                      11-MAY-1999;
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18-JUN-1
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                                      gene that codes for a novel protein (see AAW43301), designated Afclp, that mediates the removal of AAX tripeptide from CAAX proteins following prenylation. AFCI was isolated using an autocrine arrest, sensitised selection for CAAX proteases. This involved coropic expression of an a-factor in an a-cell and a CAAX permutation defective for proteelysis. Of 127 mutants isolated, 22 had mutations in a single gene (AFCI). This is the first CAAX protease to be identified. Genetic knockout of AFCI resulted in incomplete reduction of a-factor production; thereby exposing the presence of a second CAAX protease. The gene for this (see AAV17602) was named RCBI (Ras and a-factor converting enzyme). Vectors comprising the AFCI or RCBI gene, polypeptides encoded by such vectors and recombinant cells transduced with the vectors and become for inhibitors of prenylation which can be used in the treatment of Ras dependent cancers such as colorectal and exocrine pancreatic carcinomas or myeloid leukaemia.
                                                                                                                                                                                                                                                                                                     GGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
                                                                                                                                                                                                                                                                                                                          741 GGTAGACAAACTGGATAAGAGACCCAAGAAGCATAAAACTCTGTGCGACAGTGGAGACCA 682
                                                                                                                                                                                                                                                                                 0; Gaps
                              This DNA sequence comprises the yeast AFC1 (a-factor convertase)
                                                                                                                                                                                                                                                          13.9%; Score 28.6; DB 19; Length 1825; 54.2%; Pred. No. 18; tive 0; Mismatches 49; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                122 AACTICCIGIGACTAACAGGICCAIAGITITICACGACACTICCAAG 168
                                                                                                                                                                                                                                                                                                                                                                     681 TATGAAATCTGACTGCAGGACTGCATTCAATAAAGAAACGGCCATG 635
                                                                                                                                                                                                                                       Sequence 1825 BP; 570 A; 398 C; 280 G; 577 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 49570.
          Claim 11; Page 47-48; 59pp; English.
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990S-0123548.
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990S-012664.
990S-0126785.
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99US-0129845.
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Matches 58; Conservative
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19-APR-1999
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03 - AuG - 1999;
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17-AUG-1999;
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                                                                                                                                                                                                              DB 21; Length 1920;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 45033.
                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                              13.9%; Score 28.6; D
57.1%; Pred. No. 19;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                              79 ATAGAACTAAGCAACGCGATACAATTTGGGT 109
                                                                                                                                                                                                                                                                                                                  296 ACATACCTCTTTATGGAAAACCTATTAGGGT 326
                                                                                                                                                                                                                                                                                                                                                                     AAC45029 standard; DNA; 2090 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic library; bacteria; human upper airway; otitis media; sinusitis;
bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                  236 ATGGATACGTTAACTTCACCAATCCCCAAGACGCTGCAAGAGGGGATCCAAGAACTGAATT 295
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                         19 ACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                           ATAGAACTAAGCAACGCGATACAATTTGGGT 109
                                                                                                                                                                                                                                                                                                                                                   296 ACATACCTCTTTATGGAAAACCTATTAGGGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 247-263; 545pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                AAF28542 standard; DNA; 66986
                                 990S-016081S
990S-0160980
990S-0160980
990S-0160989
990S-0161404
990S-0161405
990S-0161369
99US-0160768.
99US-0160770.
99US-0160814.
                                                                                                                                                           99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                  52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis.
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                                                                                                                                                                                                                                      Similarity
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           21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                              2922 TIGGIGGCTICGGCAAAACTIGCTITAAAIGACAAGCAGGIGAGAIGACACAAGACAIG 2981
                                                                                                                                                                                                                         105 TGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTTCACGACACTTC 164
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein (ABP25413-ABP30895) from group B
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                                                                                                                                        DB 22; Length 66986;
                                                                                                   Seguence 66986 BP; 18889 A; 13427 C; 15112 G; 19558 T; 0 other;
                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                              2982 GCGGGTTGCCCCACACAATCCAAAGTTTTGATTTTC 3020
                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus polynucleotide SEQ ID NO 10967.
                                                                                                                                                                                                                                                                                                      165 CAAGGACGCCATACCGAACAAAGCAAGGTGTTATTATCC
                                                                                                                                      Score 28.6; DB
Pred. No. 68;
0; Mismatches
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                                                                                                                                                                              0;
                                                                                                                                        13.9%;
55.6%;
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                     Conservative
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                                                                                                                                                         Best Local Similarity
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                                                             and meningitis.
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Tettelin H;
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acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
                                                                              Sequence 2155561 BP; 695741 A; 385320 C; 382958 G; 691542 T; 0 other;
                                                                                                                                                                                                                                            97 ATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCAC 156
                                                                                                                                                0; Gaps
                                                                                                                                                                              37 ICAATITICCAGGACACAGATGATICGGTCCAAGAACAGGATAATAGAACTAAGCAACGCG 96
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reproductive system, chromosomal marker, forensic, urinary disorder,
chronic nephritis, blood-related disorder, thrombosis, ds.
                                                                                                            Query Match
Best Local Similarity 51.1%; Pred. No. 2.18+02;
Matches 67; Conservative 0; Mismatches 64; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human prostate cancer antigen, Seq ID No 819.
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16-MAR-2000; 2000US-0189374.
18-ARR-2000; 2000US-0199076.
18-ARR-2000; 2000US-0199076.
18-ARR-2000; 2000US-0295153.
19-MAY-2000; 2000US-0295515.
28-UUN-2000; 2000US-0215135.
30-UUN-2000; 2000US-0216486.
30-UUN-2000; 2000US-0216486.
30-UUL-2000; 2000US-0216486.
31-UUL-2000; 2000US-0216487.
07-UUL-2000; 2000US-0217487.
11-UUL-2000; 2000US-0217487.
11-UUL-2000; 2000US-0217487.
14-AUG-2000; 2000US-022513.
14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225267.
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2000US-0180628.
2000US-0184664.
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                                                                                                                                                                                                                                                                                                           157 GACACTTCCAA 167
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2000US-0231413.
2000US-0231414.
2000US-0232080.
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2000US-0231968.
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2000US-0232398.
2000US-0232399.
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2000US-0233063.
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2000US-0234223.
2000US-0234274.
2000US-0234997.
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2000US-0235484.
2000US-0235834.
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2000US-0241221
2000US-0241221
2000US-0241285
2000US-0241808
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2000US-0226868.
2000US-0227182.
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2000US-0246526.
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                                                                  22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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02-OCT-2000
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                                 14-AUG-2000;
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21-SEP-2000;
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25-SEP-2000;
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29-SEP-2000;
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The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for admening, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating preventing and/ or prognosing disorders related to the reproductive nephritis; and blood-related disorders og. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in antigen coding sequences, and related PCR primers and sequences antigen coding sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                    01-DEC-2000; 2000US-0250301.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251886.
                                                                                              2000US-0249210.
2000US-0249211.
2000US-0249212.
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                                                                                                                                                     2000US-0249214.
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08-DEC-2000; 2000US-0251869.
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17-NOV-2000;
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Human; prostate cancer antigen; cytostatic; uropathic; diagnositc; reproductive system; chromosomal marker; forensic; urinary disorder; chronic nephritis; blood-related disorder; thrombosis; ds.
                                                                                                                          DNA encoding human prostate cancer antigen, Seq ID No 820.
                  283 GIGGAAGAACAGIAAAAGIGAIIGGAIICIGGAIAIAIII 242
85 CTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT
                                                                   AAS40668 standard; DNA; 415 BP
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2000US-0225267.
2000US-0225268.
2000US-0225770.
2000US-022547.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0227182.
2000US-0227009.
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07-UNY-2000, 2000US-0209467.
28-UNY-2000, 2000US-0215185.
30-UNY-2000, 2000US-0215185.
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2000US-0184664
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16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0190076.
18-APR-2000; 2000US-0198123.
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2000US-0217487
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2000US-0225759
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2000US-0226681
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                                                                                                        17-DEC-2001 (first entry)
                                                                                                                                                                                                          WO200155316-A2.
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14-AUG-2000; 2
14-AUG-2000; 2
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14-AUG-2000;
14-AUG-2000;
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06-SEP-2000;
08-SEP-2000;
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24-FEB-2000;
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14-AUG-2000;
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                                                                                                                                                                                       Homo sapiens.
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                                                                                      AAS40668;
                                               RESULT 31
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0; Gaps

0; Mismatches 46; Indels

56; Conservative

Matches

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Best Local Similarity

343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTCTTAGGTCAGGGTGATAGCA 284

25 ACGAGTICTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAA 84

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2000US-0246610.
2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249208.
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2000US-0246478.
2000US-0246523.
                             2000US-0232080.
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2000US-0231968.
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2000US-0232399.
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2000US-0241221.
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2000US-0244617.
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2000US-0246609.
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13-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
08-NOV-2000;
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The invention relates to novel isolated human prostate cancer antigen polymuclectides (I) and polypeptides (II). (I) and (III) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis, and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AAS40061-AAS4075 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTCTTAGGTCAGGGTGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer antigen; cytostatic; uropathic; diagnositc; reproductive system; chromosomal marker; forensic; urinary disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGAGITCITGGICAATTICCAGGACACAGATGATICGGICCAAGAACAGGATAATAGAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; Score 28.4; DB 22; Length 415; 54.9%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human prostate cancer antigen, Seq ID No 821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 CTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID No 820; 546pp; English
                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Barash SC, Ruben SM;
                                                                     2000US-0249300.
2000US-0250160.
2000US-0250391.
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                                 2000US-0249297.
2000US-0249299.
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2000US-0251479.
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08-DEC-2000; 2000US-0251869.
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08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
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es 56; Conservat
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01-DEC-2000;
05-DEC-2000;
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ID AAS4064
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chronic nephritis; blood-related disorder; thrombosis; ds
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2000US-0216880.
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2000US-0217496.
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2000US-0225759.
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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26-JUL-2000)
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11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                 Homo sapiens
                                              02-AUG-2001
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RR 25-SEP-2000; 2000US-0234998.

RR 26-SEP-2000; 2000US-0235484.

RR 29-SEP-2000; 2000US-0235484.

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RR 29-SEP-2000; 2000US-0235487.

RR 29-SEP-2000; 2000US-0236569.

RR 20-CCT-2000; 2000US-0236569.

RR 20-CCT-2000; 2000US-0237039.

RR 20-CCT-2000; 2000US-0237039.

RR 20-CCT-2000; 2000US-0237039.

RR 20-CCT-2000; 2000US-0241785.

RR 20-CCT-2000; 2000US-024186.

RR 20-CCT-2000; 2000US-024186.

RR 20-CCT-2000; 2000US-024186.

RR 20-CCT-2000; 2000US-0246477.

RR 20-CCT-2000; 2000US-0246527.

RR 17-NOV-2000; 2000US-0246527.

RR 17-NOV-2000; 2000US-0246527.

RR 17-NOV-2000; 2000US-0249221.

RR 17-NOV-2000; 2000US-024921.

RR 17-NOV-2000; 2000US-024

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The invention relates to novel isolated human prostate cancer antigen polymucleotides (I) and polypeptides (II). (I) and (II) are useful for polymucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and, or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chromic neptritis, and blood-related disorders e.g. thrombosins. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunosassays. AAS40061-AAS40775 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form invention. Note: The sequence data for this patent did not form the printed specification, but was obtained in electronic format cancer and invention are fifp.wipo.int/pub/published_pct_sequences.
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                                                                                 Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                       343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTTCTTAGGTCAGGGTGATAATGT 284
                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   25 ACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 9243.
                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 28.4; DB 22; Length 415; 54.9%; Pred. No. 13; tive 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                             Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 CTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 GTGGAAGAACAGTAAAAAGTGATTGGATTCTGGATATTT 242
                                                                                                                                  Disclosure; SEQ ID No 821; 546pp; English
                                      Ruben SM;
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            (HUMA-) HUMAN GENOME SCI INC.
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2000US-0184664.
2000US-0186350.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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                                   Barash SC,
                                                           WPI; 2001-451929/48.
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nes 56; Conserv
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24-FEB-2000;
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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                                    Rosen CA,
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2000US-0229345.
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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1-SEP-2000;
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Ruben SM,
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                                                                          -NOV-2000;
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition

Disclosure; SEQ ID NO 9243; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.

Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

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0
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Score 28.4; DB; Pred. No. 13; 0; Mismatches
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ilarity 54.9%;
Conservative (
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Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTCTTTAGGTCAGGGTGATAGCA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 ACGAGTICTIGGICAATTICCAGGACACAGATGATICGGICCAAGAACAGGATAATAGAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9244; 1297pp + Sequence Listing; English.
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Homo sapiens

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Barash SC, Ruben SM;

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P-PSDB; AAR15471.
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                RESULT 37
Db
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                                                                        The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                          Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                          343 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTGTCTTAGGTCAGGCTGATAGCA 284
                                                                                                                                                                       Gaps
                                                                                                                                                                                        25 ACGAGITCITGGICAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAA 84
                                     is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                      .;
0
                                                      Disclosure; SEQ ID NO 9245; 1297pp + Sequence Listing; English.
                                                                                                                                                 Query Match 13.8%; Score 28.4; DB 22; Length 415; Best Local Similarity 54.9%; Pred. No. 13; Matches 56; Conservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                      Signal peptide; promoter; transcription control; protease; IFN; IL; EGF; GM-CSF; Factor VIII; insulin; TNF; NGF; vector; foreign protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/label= transcription_control_region
note= "claim 6, page 29"
                                                                                                                                 Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
                                                                                                                                                                                                                             85 CTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTT 126
                                                                                                                                                                                                                                              283 GİGGAAGAAAÇAĞİAAAAĞİĞATİĞĞATİCTGGATATATİ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
note= "claim 5, page 29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hashimoto T, Tsujimura A, Udaka J;
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                             AAQ15229 standard; DNA; 1796 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/label= BBRP42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-JP00626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90JP-0122166
                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARH ) HOECHST JAPAN LTD.
                                                                                                               protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
        WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-369253/50
                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1990;
                                                                                                                                                                                                                                                                                                                                  11-MAR-1992
                                                                                                                                                                                                                                                                                                                                                    BBRP42 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9118101-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_signal
                                                                                                                                                                                                                                                                                                                 AAQ15229;
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                     AAQ15229/c
                                                                                                                                                                                                                                                                           RESULT 36
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                                                                                                                                                                    DNA encoding the signal peptide associated with the BBRP42 gene of B. brevis may be incorporated into an expression vector, pref. with the promoter sequence and transcription control region as indicated in the features. DNA encoding a foreign protein may be ligated immediately downstream of the signal region. The vector may then be used to transform a host organism which then expresses the protein on culture. BRRP42 is secreted by B. brevis during an early stage of incubation, and so its associated signal peptide allows a foreign protein to be secreted during this early stage when protease prodn. is low, thus increasing recovery of the protein. Proteins for which the method may be used include interferon, interleukin, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 TTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 TTGGAGTTTATCGGCATCCAGCTTCAAGAGAGACAGCAGTTCTTCGTTTTTTCTCGAAGCC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
Expression vector for signal peptide from Bacillus brevis - for expression of interferon, insulin, epidermal growth factor etc. with improved yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 28.4; DB 12; Length 1796; 58.1%; Pred. No. 21; tive 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermal growth factor, GM-CSF, Factor VIII, insulin, tumour necrosis factor and NGF.
See also AAQ15229-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1796 BP; 603 A; 359 C; 490 G; 344 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C glutamicum coding sequence fragment SEQ ID NO: 2176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizoguchi H, Ando S, Hayash
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                  Disclosure; Fig 3A-B; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 TCCAAGGACGCCATACCGAACAAGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 ACCGATGAAGCCTCCTCTGCCGAAGC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH67141 standard; DNA; 3012 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0377484.
2000JP-0159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 58.1
nes 50, Conservative
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07-APR-2000;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2001.
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                                                                                                                                                                                                           These
                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 15421.
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                                                                                                  Claim 8; SEQ ID NO: 2176; 246pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3012 BP; 676 A; 877 C; 891 G; 568 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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60.3%; Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1658 CGATCACCTTCCTGGATA 1675
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL21316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                               48 GACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGG 107
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a coat protein gene of barley mild mosaic virus (BaMMV). The determ. of the genetic structure of BaMMV coat proteins may contribute to the diagnosis of the virus which causes barley yellow mosaic disease, as well as to the prodn. of yellow mosaic-disease, as well as to the prodn. of yellow mosaic-disease resistant barley utilising BaMMV coat protein
                                                                                                                                                                                                                                                                                           108 GIGGATIGGCAACAAACTICCIGIGACTAACAGGICCATAGITITICACGACACTICC 165
                                                                                                                                                                                                                                                                                                                       820 AACGAAAATAAATAAACCCGTTGCCATTGACTAAACTTTTACAAGAGATTTTC 763
           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mild mosaic virus; diagnosis; barley yellow mosaic disease;
cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA sequences encoding barley mild mosaic virus coat protein - useful for diagnosis and prepn. of resistant strains
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0
                                                                                                                                                                   DB 23; Length 3045;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "BaMMV strain Kal coat protein"
                                                                                                                                    Sequence 3045 BP; 856 A; 726 C; 698 G; 765 T; 0 other;
                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuroda H;
                                                                                                                                                                   Score 28.4; DE
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mosaic virus strain Kal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kashiwazaki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NORQ ) JAPAN MIN AGRIC FORESTRY. (SAPB ) SAPPORO BREWERIES.
                                                                                                                                                                     13.8%;
52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      AAQ53462 standard; DNA; 3946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92JP-0180624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..3609
/*tag= a
2854..3606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease resistant barley;
                                                                                                                                                                                  Best Local Similarity 52.5
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BaMMV coat protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-407253/51.
                                                             (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hibino H, Ito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR44507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barley mild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP574878-A
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ53462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc RNA
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes.
                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                           AAQ53462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                    Gaps
                                                                                                                                  612 AGGCATGACCATGAAACCCATGAGTTCTTTCACCATTGACAGCGCAAAGATGGTTGGCTT 671
                                                                                                  6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTTCCAGGACACAGATGATTCGGTC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genomic polynucleotide SEQ ID NO 15415.
                                 13.8%; Score 28.4; DB 14; Length 3946; 54.9%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 15415; 21pp + Sequence Listing; English.
                                                                    Indels
Sequence 3946 BP; 1110 A; 1059 C; 891 G; 886 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4407 BP; 1332 A; 955 C; 917 G; 1203 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                   66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGG 107
                                                                                                                                                                                                   672 CATCAAGACCGCAAAAGACACCTCAACTGCATCCTTTACGG 713
                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 28.4; DB 23; 52.5%; Pred. No. 30;
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                     ABL21314 standard; DNA; 4407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                      Query Match
Best Local Similarity 54.99
Marches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
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Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions -
                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                       ABL21314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                       ABL21314/c
                                                                                                                                                                                                                                                      RESULT 40
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These
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 295126 GCATTACCCAGGGGCATTGGTGCATACCAGGTCAAGGTAAATGTCGAGGACGCACTGAGCGCA 295067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                  3666 AACGAAAATAAATAAACCCGTTGCCATTGACTAAACTTTTACAAGAGATTTTC 3609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
108 GTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 349980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO: 7065; 246pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                  C glutamicum coding sequence fragment SEQ ID NO: 7065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 28.4; DB 22; 60.3%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
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                                                                                                                                 AAH68530 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-2000; 2000JP-0159162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0377484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                             organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum.
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CGGTCCAAGAACAGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                            26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                   EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                       AAH68530;
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                                                                                                               AAH68530/
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Db 295066 CGATCACCTTCCTGGATA 295049

. 3726 GATACCAAGTATTCATTCATAAAACTGTAAACTGGCACCCACGCCCACGAAATAATTCGA 3667

48 GACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGG 107

Indels

26;

0; Mismatches

Conservative

6

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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or poly4+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the same obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain
                                                                                                                                                                                                                                                                                                                          sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 CTIGITGICAACACAGAIGAICCCCAGGICAAATIICIGCACTCCTAAAATCCICCTIAC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGATGGGGATGACTCGCTGCAGATTTCT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upstream regulatory sequences and to design expression and secretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 383 BP; 100 A; 82 C; 88 G; 111 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 1802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 1802; 71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                                                                                                                            gene therapy; chromosome mapping; ss.
                                                             AAC01804 standard; cDNA; 383 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%;
51.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122487
                                                                                                                                                                                        06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                          expressed
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                                                                                                                                                                                                                                                                                                                       Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                           AAC01804;
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                                  AAC01804/c
RESULT 42
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This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) percoded by (A) are used. (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AZ33477-Z33540 represent expressed sequence tags described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                              Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 GAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGATGGGGATGACTCGCTGCAGATTTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 CTTGTTGTCAACACAGATGATCCCCAGGTCAAATTTCTGCACTCCTAAAATCCTCCTTAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                        Dahl E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                        Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28.2; DB; Pred. No. 16; 0; Mismatches
                                                                                                Human prostate cancer-associated EST 31,
                                                                                                                                                                                                                                                                                                                                                       (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK99319 standard; cDNA; 652 BP.
AAZ33507 standard; cDNA; 501 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim la; 99; 194pp; German.
                                                                                                                                                                                                                                                                                      98DE-1011194
                                                                                                                                                                                                                                                                                                                         98DE-1011194
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 1999-519629/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 TGTGACTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AATCACCAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY48371.
                                                                                                                                                                                                                      DE19811194-A1
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                         10-MAR-1998;
                                                                  08-DEC-1999
                                                                                                                                                                                                                                                                                        10-MAR-1998;
                                                                                                                                                                                                                                                      16-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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                               AAZ33507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agents
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ID AAK9
XX
AC AAK9
XX
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RESULT 43 AAZ33507/c

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                                         Ferritin 14 protein; DNA recombination; antagonist; malignant tumour; haemopathy; HIV infection; immunological disease; inflammation; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel ferritin 14 protein, the encoding polynucleotide, the production of the polynucleotide using DNA recombination, and an antagonist against the polynucleotide. The polynucleotide of the invention is useful for curing diseases such as malignant tumours, haemopathy, HIV infections, immunological disease and various inflammations. This polynucleotide sequence represents the CDNA encoding the ferritin 14 protein of the invention.
                                                                                                                                                                                                                                                                                                        Polypeptide ferritin 14, for curing diseases such as malignant tumor, hemopathy, HIV infection, immunological disease and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 CTIGITGICAACACAGAIGAICCCCAGGICAAATITCIGCACICCIAAAATCCICCIIAC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGATGGGGGATGACTCGCTGCAGATTTCT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.7%; Score 28.2; DB 24; Length 652; 51.2%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 652 BP; 140 A; 174 C; 202 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein encoding cDNA sequence SEQ ID NO:599.
                                                                                                                            /product= "Protein of ferritin 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 24 Disclosure; 31pp; Chinese.
                                                                                                                                                                                                                                (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                            Location/Qualifiers
                    cDNA encoding ferritin 14 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH99764 standard; cDNA; 716 BP.
                                                                                                                                                                                        24-MAY-2000; 2000CN-0115822
                                                                                                                                                                                                              24-MAY-2000; 2000CN-0115822
11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 51.2
Matches 66; Conservative
                                                                                                       193..567
                                                                                                                                                                                                                                                                           WPI; 2002-281644/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 TGTGACTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 AATCACCAA 199
                                                                                                                                                                                                                                                                                     P-PSDB; AAO20447
                                                                                                                                                                                                                                                                                                                              inflammations -
                                                                                                                                                                                                                                                      Mao Y, Xie Y;
                                                                        Unidentified
                                                                                                                                               CN1324811-A.
                                                                                                                                                                    05-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH99764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 45
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antidabetic; oftostatic; neuroprotective; antidepressant; nockropic; antidabetic; oftostatic; neuroprotective; antidepressant; nockropic; antiparkinsonian; and immunostimulant. The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphlaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiavascular; antianaemic; anaemia; anti-Hry, fungicate; antimateagen; cardiavascular; antianaemic; eczema; dermatological; hatialergic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialergic; antiseshmatic; antidabetic; cytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflection; immunostimulant; rheumatod arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteopotetic disorder; platelet disorder; asthma; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25931. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antirhoumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 crigirigicaacacagargarccccaggicaaarircrgcacrccraaaarccrccrrac 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 634; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM25823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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09-833799-13c.rng

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(RetinaXR) polypeptide with antidiabetic, anorectic, ophthalmological, antigout, antinflammatory and immunostimulant activity. RetinaXR is useful for screening a compound for its ability to inhibit or activate RetinaXR nuclear receptor, as a diagnostic agent for diagnosing patients having a predisposition to diabetes and/or obesity, for monitoring patient's response to treatment of diabetes or obesity, for treating a subject having a disorder that is responsive to RetinaXR receptor modulation e.g. diabetes, obesity and age-related macular degeneration, for treating retinopathies e.g. diabetic retinopathy, conjunctivitis, DiGeorge's syndrome, retinitis pigmentosa, neovascular glaucoma, corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= b 'note= "Encodes the amino-terminal A/B domain, claim 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, RetinaXR, antidiabetic, anorectic, ophthalmological, antigout, antiinflammatory, immunostimulant, nuclear receptor; diabetes; obesity, age-related macular degeneration, retinopathy, conjunctivitis, gout, bigeorge's syndrome, retinitis pigmentosa, neovascular glaucoma, corneal inflammation, severe combined immunodeficiency disease; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nuclear receptor, RetinaX receptor
563 AATCTCGATCTTACTGCGAAGTGGCGCTCTCCTGATGGGGATGACTCGCTGCAGATTTCT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "Encodes the ligand binding domain, claim 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nuclear receptor, RetinaX receptor polypeptide, useful for identifying modulators of the receptor which are used for treating diabetes, obesity, age-related macular degeneration, gout,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= c
note= "Encodes the DNA binding domain, claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatomyositis; gene therapy; gene expression; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human RetinaXR encoding cDNA SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /"tag= a
/product= "RetinaXR"
19..156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 28; 30pp; English.
                                                                                                                                                                                                                                                                                                ABA05428 standard; cDNA; 1514 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2001; 2001WO-US14601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352..1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-049337/06.
                                                                  129 TGTGACTAA 137
                                                                                                                                  623 AATCACCAA 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2002
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inflammation, severe combined immunodeficiency disease, gout, defantacmyositis, etc. Nucleic acids encoding RetinaXR are also useful for treating the above mentioned disorders by gene therapy. The present sequence is that of the RetinaXR encoding CDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a consensus RACE sequence of human retinal orphan nuclear hormone receptor variants heetinOR2 and heetinOR1. The two heetinOR polynucleotides are identical, except that heetinOR2 includes a 40 bp insertion following nucleotide 1188. This insertion, which is due to a mRNA splicing variation, introduces a stop codon into polypeptide. The polynucleotide, which results in a truncated heetinOR2 polypeptide. The polynucleotides are expressed only in the retinal tissues. The nuclear hormone receptors are found in retinal cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are useful for identifying ligands that can modulate their activity and for identifying response elements that are responsive to the nuclear hormone receptors. The receptors and methods are useful for research of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human retinal nuclear hormone receptor and coding sequences, useful for identifying ligands and response elements involved in homeostasis -
                                                                                                                                                                                                                                                             1462 TACCACAACTIGITIAAITICAICCIACCAICAATAIACAGITITIGGGGCTAITAIGAATAAA 1403
                                                                                                                                                                                                                         64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; retinal orphan nuclear hormone receptor; splice variant;
                                                                                                                                       13.7%; Score 28.2; DB 24; Length 1514; 57.3%; Pred. No. 24; ive 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28.2; DB 21; Length 1920; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human retinal nuclear receptor consensus RACE sequence.
                                                                                                      Sequence 1514 BP; 352 A; 446 C; 424 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1920 BP; 480 A; 514 C; 536 G; 390 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response element; ss.
                                                                                                                                                                                                                                                                                                                                              1402 GCTGCTATGAATATTCTTACAATATCTTT 1374
                                                                                                                                                                                                                                                                                                        124 CTTCCTGTGACTAACAGGTCCATAGTTTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ61225 standard; DNA; 1920 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hRetinOR2; hRetinOR1; retina;
hormone-mediated homeostasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone-mediated homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US17885
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                                                                                                                                                                               Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De La Brousse-Elwood FC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TULA-) TULARIK INC.
                                                                                                                                            Query Match
Best Local Similarity
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57.3%;

Best Local Similarity

Query Match

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0; Gaps

Indels

0; Mismatches 38;

Score 28.2; DB 21; Length 1931; Pred. No. 26;

13.7%; 57.3%;

51; Conservative

Matches

Local Similarity

Query Match

64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123

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The present sequence encodes a human retinal orphan nuclear hormone receptor variant, designated hRetinOR1. The specification also describes variant hRetinOR2. The two hRetinOR polynucleotides are identical, except that hRetinOR2 includes a 40 bp insertion following nucleotide 1188. This insertion, which is due to a mRNA splicing variation, introduces a stop codon into the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2 polypeptide. The polynucleotides are expressed only in the retinal tissues. The nuclear hormone receptors are found in retinal cells, and are useful for identifying ligands that can modulate their activity and for identifying response elements that are responsive to the nuclear hormone receptors. The receptors and methods are useful for research of hormone-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human retinal nuclear hormone receptor and coding sequences, useful for identifying ligands and response elements involved in homeostasis
                                                        1531 TACCACAACTITATTATTCATCCTACCATCAATATACAGTTTGGGGCTATTATGAATAAA 1472
                             64 TCCAAGAACAGGATAATAGAACTAAGGAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
0; Gaps
                                                                                                                                                                                                                                                                                                                                                      Human; retinal orphan nuclear hormone receptor; splice variant;
                                                                                                                                                                                                                                                                                                                    DNA encoding human retinal nuclear receptor variant hRetinOR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl except= (pos: 103..105, aa: Arg)
/transl_except= (pos: 241..243, aa: Cys)
/transl_except= (pos: 331..335, aa: Thr)
/transl_except= (pos: 607..609, aa: Glu)
/transl_except= (pos: 868..870, aa: Glu)
/transl_except= (pos: 1019..1021 aa: Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1931 BP; 473 A; 517 C; 538 G; 387 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (pos: 241..243, aa: Arg)
(pos: 241..243, aa: Cys)
(pos: 331..335, aa: Thr)
 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor"
                                                                                                                                                                                                                                                                                                                                                                         hRetinOR2; hRetinOR1; retina; response element; hormone-mediated homeostasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product= "retinal nuclear
     0; Mismatches
                                                                                                                                      1471 GCTGCTATGAATATTCTTACAATATCTTT 1443
                                                                                                      124 CTTCCTGTGACTAACAGGTCCATAGTTTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Fig 1; 58pp; English.
                                                                                                                                                                                                                AAZ61224/c
ID AAZ61224 standard; DNA; 1931 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US17885
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..1206
        51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-195554/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                               30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000
                                                                                                                                                                                                                                                                 AAZ61224;
              Matches
                                                                                                                                                                                              RESULT 48
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The present sequence encodes a human retinal orphan nuclear hormone receptor variant, designated hRetinOR2. The specification also describes variant hRetinOR1. The two hRetinOR polynucleotides are defentional, except that hRetinOR2 includes a 40 bp insertion following nucleotide 1188. This insertion, which is due to a mRNA splicing variation, introduces a stop codon into the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2 polypeptide. The polynucleotides are expressed only in the retinal tissues. The nuclear hormone receptors are found in retinal cells, and are useful for identifying ligands that can modulate their activity and for identifying response elements that are responsive to the nuclear hormone receptors. The receptors and methods are useful for research of hormone-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human retinal nuclear hormone receptor and coding sequences, useful for identifying ligands and response elements involved in homeostasis
1531 raccacactrintarircarccraccarcaararacagrificagecrafrargaaraa 1472
                                                                                                                                                                                                                                                                                         Human; retinal orphan nuclear hormone receptor; splice variant;
                                                                                                                                                                                                                                                         DNA encoding human retinal nuclear receptor variant hRetinOR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= (pos: 103..105, aa: Arg)
/transl_except= (pos: 241..243, aa: Cys)
/transl_except= (pos: 331..335, aa: Thr)
/transl_except= (pos: 607..609, aa: Glu)
/transl_except= (pos: 868..870, aa: Glu)
/transl_except= (pos: 1019..1021 aa: Leu)
                                                                                                                                                                                                                                                                                                          hRetinOR2; hRetinOR1; retina; response element; hormone-mediated homeostasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear
                                                                        1471 GCTGCTATGAATATTCTTACAATATCTTT 1443
                                        124 CTTCCTGTGACTAACAGGTCCATAGTTTT 152
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product= "retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Fig 1; 58pp; English.
                                                                                                                                                             AAZ61223 standard; DNA; 1960 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human retinal nuclear hormone receptor and coding sequences, useful for identifying ligands and response elements involved in homeostasis -
                                                                                                                                                                      1571 TACCACAACTIGTIAATICATCCTACCATCAATATACAGTTIGGGGGCTATIATGAATAAA 1512
                                                                                                                                    TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; retinal orphan nuclear hormone receptor; splice variant;
                                                                      Length 1960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
13.7%; Score 28.2; DB 21; Length 1978;
Best Local Similarity 57.3%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 38; Indels 0;
                                                                                                     Indels
                                Sequence 1960 BP; 480 A; 523 C; 539 G; 401 T; 17 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1978 BP; 475 A; 528 C; 536 G; 398 T; 41 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human retinal nuclear receptor consensus DNA sequence.
                                                                                                   38;
                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response element;
                                                                  Score 28.2; DB
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                           1511 GCTGCTATGAATATTCTTACAATATCTTT 1483
                                                                                                                                                                                                        124 CTICCIGIGACIAACAGGICCAIAGITIT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hRetinOR2; hRetinOR1; retina; res
hormone-mediated homeostasis; ss.
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                                                                                                                                                                                                                                                                                                                              AAZ61236 standard; DNA; 1978
                                                               Query Match
Best Local Similarity 57.3%;
Matches 51; Conservative
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homeostasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raccoon poxvirus; RCNV; thymidine kinase; TK; vaccine; haemagglutinin; HA; feline pathogen; feline panleukopenia virus; FPV; feline calcivirus; FCV; capsid protein; virucide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poxviruses are useful as vaccines to immunise felines against subsequent challenge by feline pathogens. The recombinant multivalent vaccine is formed by inserting multiple genes such as a feline panleukopenia virus (FPV) gene, and/or a feline calcivirus (FCV) capsid protein gene each operably linked to a promoter, into a raccoon poxvirus for expression. The present sequence is Feline calcivirus (FCV) capsid protein encoding
1571 TACCACAACTTGTTAATTCATCCTACCATCAATATACAGTTTGGGGCTATTATGAATAAA 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New multivalent recombinant raccoon poxviruses, useful as vaccines to immunize felines against subsequent challenge by feline pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 ATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AGGATAACAACATTAAAGGGTTATCGCAGAAGCCAACATGTAGAAATTTGTTGGGGTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          poxviruses (RCNV), containing more than one exogenous gene inserted into either the thymidine kinase (TK) gene, the haemagglutinin (HA) gene, or a combination thereof. The multivalent recombinant raccoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /+tag= a
/product= "Feline calcivirus (FCV) capsid protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to multivalent recombinant raccoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2007 BP; 528 A; 473 C; 421 G; 585 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Esposito JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                        1511 GCTGCTATGAATATTCTTACAATATCTTT 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Column 31-36; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feline calcivirus (FCV) capsid gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                           124 CTTCCTGTGACTAACAGGTCCATAGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hu L,
                                                                                                                                                                                                                                                                                                         AAD08548 standard; DNA; 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0552369.
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                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scott FW, Ngichabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-407214/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline calcivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAE04304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1991;
27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6241989-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                      AAD08548;
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Gaps

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64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123

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AAQ94444;
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                      RESULT 53
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                                       AAQ94444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRFK cells were inoculated, total poly-A+ RNA was isolated and FCV double-stranded RNA was LiCl fractionated from this RNA. Double-stranded cDNA was prepared, blunt-ended with t4 DNA polymerase and treated with EcoRI methylase prior to ligation of EcoRI linkers. The treated with EcoRI methylase prior to ligated to lambda gtl0. E.coli mixture was digested with EcoRI and ligated to lambda gtl0. E.coli strains transformed with the viral vectors were plated and positive plaques were transferred to nitrocliulose. They were probed with a random-primed cDNA prepared from FCV genomic RNA. A plaque with a strong hybridisation signal was isolated and found to contain an a second library was constructed in pUC18 to give pCV2. EcoRI fragment (ca.4200bp). It was cloned in pUC18 to give pCV2. These two plasmid was selected from this library and designated pCV7. It was conduct to have restriction sites in common with pCV2. These two plasmids were used to isolate other regions of the FCV genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 ATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 AGGATAACAACATTAAAGGGTTATCGCAGAAGCCAAACATGTAGAAATTTGTGGGGTT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feline calcivirus capsid protein - from recombinant DNA for subunit and multivalent vaccines for FCV
                                                                                                                                                                                                                                  feline calcivirus capsid protein; PCV; multivalent vaccine; cat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 2385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 GGCAACAACTICCTGTGACTAACAGGTCCATAGTTTTTCACGAC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2385 BP; 642 A; 562 C; 502 G; 679 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 GÁTTACCAATTTGATGTGAGGATCCCAATCATAGTATTTAAGCAC 39
115 GGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGAC 159
                  Score 28.2; DB; Pred. No. 28; 0; Mismatches
                                                                                                                                                                                                             Encodes Feline calcivirus capsid protein.
                                                                                                                                                                                                                                                                                                                                                     /product= capsid protein
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 28; 40pp; English.
                                                                                                                 AAQ10484 standard; cDNA; 2385 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%;
54.3%;
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                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       18..2024
/*tag= a
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-058117/08.
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                                                                                                                                                                                                                                                                             feline calcivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR10686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wardley R,
                                                                                                                                                                                  22-APR-1991
                                                                                                                                                      AAQ10484;
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                                                                                        RESULT 52
AAQ10484/c
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The present DNA shows the transferrin receptor (TfR) operon consisting of two genes (Tpp1 and Tbp2) arranged in tandem and which are transcribed trom a single promoter, from Haemophilus influenzae type b, strain MinnA. H. influenzae TfR is iron- and/or haemin-regulated and a putative furble binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the TfR is that it shares homology with TfR of other H. influenzae strains including non-typable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579 İTCTİATİAGGİCACGIACİCCCAAĞĞACĞACAİACÇIAAAACAĞĞAAĞIGCAAAAİA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 TCCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGITATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                     Bacterial transferrin receptor operon (H. influenzae strain MinnA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of Haemophilus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harkness R, Klein M, Loosmore S;
                                                                                                                                                                                         Tbpl; Tbp2; transferrin receptor operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 5A-Q; 231pp; English.
                                                                                                                                                                                                                                                                      Haemophilus influenzae strain MinnA.
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang Y;
AAQ94444 standard; DNA; 5009 BP.
                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= Tbp2
2117..4856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= Tbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.78;
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Les 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= b
                                                                                                                                                                                                                                                                                                                                                   121..2103
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Murdin A, Schryvers A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-194089/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR77887-88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 CCTAG 206
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08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9513370-A1
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Gaps

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23; Indels

0; Mismatches

42; Conservative

Matches

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Hemophilus influenzae type b, strain MinnA. The bacterial transferrin receptor is composed of 2 chains, Topl and Top2. Hinfluenzae is a non-typable bacterium responsible for a wide range of human diseases. Iron is an essential nutrient for the growth of these of human diseases. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. The Holl length Top2 protein is produced in low amounts in Escherichia coli. However, the yield can be enhanced by truncation of the 3' end of the gane. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a manigen in immunoassays for the detection of theme produced as a manigen in immunoassays for the detection of tender transferrin receptor
                                                                                                                                                                                                                                                                                                                                                    Transferrin receptor; Haemophilus influenzae type b;
iron; human transferrin; iron source; antibody; bacterial growth;
vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents the transferrin receptor gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus truncated transferrin receptor protein analogue, Tbp
used to induce protection against disease caused by transferrin
producing pathogens, or as antigen to detect Haemophilus TfR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore SM;
                                                                                                                                                                                                                                                                                     Transferrin receptor gene sequence encoding Tbp1 and Tbp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2117.4855
/*tag= b
/note= "encodes Tbp1 (AAW08961)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121..2103 -
/*tag= a
/note= "encodes Tbp2 (AAW08962)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harkness RE,
, Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                   AAT49502 standard; DNA; 5009 BP.
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95US-0483577.
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murdin AD, Schryvers AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray-Owen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW08961-62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052329/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1996;
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                                                                                                                                                                                                                 05-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1996
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                                                                                                                                              AAT49502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chong P,
RESULT 54
                                         AAT49502
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1579 TICTTATTAGGICACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAATAT 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The H. influenzae transferrin receptor operon contains two genes (tbpl and tbp2) under the transcriptional regulation of one promoter. The proteins encoded from these genes can be expressed in a recombinant host. The proteins can be used in vaccines against H. influenzae infections or to produce antibodies for use in diagnosis or passive
142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purification of recombinant Haemophilus transferrin-binding protein - by solubilising inclusion bodies separated from cell lysate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.6%; Pred. No. 36;
Matches 42; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loosmore S;
                                                                                                                                                                                                                                          tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
                                                                                                                                                                                                                H. influenzae strain Minn A transferrin receptor operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harkness R,
Yang Y;
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                         AAV21430 standard; cDNA; 5009 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 5; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/product= Tbp2
                                                                                                                                                                                                                                                                                                                                               /product= Tbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0148968.
93US-0175116.
95US-0487890.
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                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                     121..2103
                                                                                                                                                                                                                                                      passive immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schryvers A,
                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray-Owen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-100410/09
                                                                           1639 CATGG 1643
                                                   CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunisation.
                                                                                                                                                                                        20-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           US5708149-A.
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                                                                                                                                                                AAV21430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chong P,
                                                  202
                                                                                                               RESULT 55
                                                                                                                           AAV21430
                                                                                                                                                                                                                                                                                                         Key
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0; Gaps

142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGTGTTATTAT 201

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13.7%; Score 28.2; DB 18; Length 5009; 64.6%; Pred. No. 36;

Query Match Best Local Similarity

Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;

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0; Gaps

23; Indels

0; Mismatches

Conservative

AAZ89158

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g δ

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42;
   Matches
                                                                                                                                                               RESULT 57
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                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                AAZ91000
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                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae which has antibacterial activity. (I) are used for recombinant production of truncated Tbp; as probes and primers for detecting, and diagnosing infection by, Haemophilus, also for isolating similar sequences from other bacteria; as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g. infections caused by bacteria that produce transferrin receptors, e.g. Haemophilus, Neisseria or Branhamella. The truncated proteins are useful as immunogens (as above); for diagnosing infection (as antigens in immunoassays) and for raising antibodies, used for diagnosis of infections or for passive immunization. This sequence encodes the transferrin receptor proteins Tbp1 and Tbp2 isolated from H. influenzae
                                                                                                                                                                                                                                                            Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding truncated transferrin receptor, useful for diagnosis, treatment and prevention of bacterial infections, particularly by Haemophilus
      1579 ITCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1638
                                                                                                                                                                                                                                 H. influenzae type B strain MinnA DNA containing Tbp1 and Tbp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray-Owen S, Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Column 65-76; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schryvers A,
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              *tag= a
product= "Tbp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Tbp2"
                                                                                                                                                 AAZ89158 standard; DNA; 5009 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chong P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0337483.
93US-0148968.
93US-0175116.
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/*tag= b
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                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                21..2103
                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type B strain MinnA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-181144/16
                                                                              1639 CATGG 1643
                                              202 CCTAG 206
                                                                                                                                                                                                                                                                                         diagnosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6015688-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2000
                                                                                                                                                                                                                13-JUN-2000
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                                                                                                                                                                                    AAZ89158;
                                                                                                                           RESULT 56
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DB 21; Length 5009;

13.7%; Score 28.2; 1 64.6%; Pred. No. 36;

Query Match Best Local Similarity

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specific for single transferin receptor proteins (or immunogenic fragment) from strains of Haemophilus influenzae. This sequence fragment) from strains of Haemophilus influenzae. This sequence for the Topi and Topi transferin receptor proteins from H. influenzae type B strain MirnA. The antibodies may be used for preventing and treating inflections and disorders caused may be used for preventing and treating influenzae including bacterial meningitis, othics media. By H. influenzae, including bacterial meningitis, othics media, be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies specific for transferrin receptor proteins of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel antibodies (or monospecific antisera)
                                                       1579 irctratraggreacgracteccaaggacacaraceraaacaggaagrgeaaaraiar 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ds.
142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. influenzae type B strain MinnA transferrin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Tbp2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "Tbp1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             AAZ91000 standard; DNA; 5009 BP.
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93US-0175116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schryvers A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-096387/08
                                                                                                                                                                                              1639 CATGG 1643
                                                                                                                                          202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6008326-A.
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                                                                                                                                                                                                                                                                                                                                                                                                AAZ91000;
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Best Local Similarity

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                                                                                         1579 Trcriariaggicaccgracicccaaggacgacaraccraaaacaggaagrgcaaaarar 1638
                                                            TCCATAGITTITCACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                    Gaps
                                                                                                                                                                                                                                                                                                                         Bacterial transferrin receptor operon (H. influenzae strain Eagan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of Haemophilus infection.
                                   ;
0
   DB 21; Length 5009;
                                                                                                                                                                                                                                                                                                                                                      Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein M, Loosmore S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5033 BP; 1822 A; 840 C; 937 G; 1434 T; 0 other;
13.7%; Score 28.2; Dilarity 64.6%; Pred. No. 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harkness R,
Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae strain Eagan.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 4A-Q; 231pp; English.
                                                                                                                                                                                                                                AAQ94443 standard; DNA; 5033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/product= Tbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-CA00616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2165..4904
                                                                                                                                                                                                                                                                                           09-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                169..2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chong P, Gray-owen S,
Murdin A, Schryvers A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-194089/25.
P-PSDB; AAR77885-86.
 Query Match
Best Local Similarity
                                                                                                                                                     1639 CATGG 1643
                                                                                                                       202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1993;
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                              42;
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                                                                                                                                                                                                                                                              AAQ94443;
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                                                              142
                               Matches
                                                                                                                                                                                                   RESULT 58
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Length 5033;

DB 16;

13.7%; Score 28.2;

Query Match

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                                                                               1627 TTCTTATTAGGTCACGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
                                                 142 TCCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGITAITAT 201
                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               growth;
                                                                                                                                                                                                                                                                                                                                                                                            iron; human transferrin; iron source; antibody; bacterial growth;
vaccine; immunogenic truncated analogue; antigen; Tbpl; Tbp2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus truncated transferrin receptor protein analogue, Tbr
used to induce protection against disease caused by transferrin
producing pathogens, or as antigen to detect Haemophilus TfR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harkness RE, Klein MH, Loosmore SM;
Yang Y;
                                                                                                                                                                                                                                                                                                                                        Transferrin receptor gene sequence encoding Tbpl and Tbp2.
                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                        Transferrin receptor; Haemophilus influenzae type b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "encodes Tbp2 (AAW08960)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "encodes Tbp1 (AAW08959)"
               0; Mismatches
64.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 4A-Q; 228pp; English.
                                                                                                                                                                                                                                     AAT49501 standard; DNA; 5033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-CA00399.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2129..4903
                                                                                                                                                                                                                                                                                                       05-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONN-) CONNAUGHT LAB LTD.
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169..2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murdin AD, Schryvers AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray-Owen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052329/05.
P-PSDB; AAW08959-60.
                                                                                                                                                    1687 CATGG 1691
                                                                                                                 202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9640929-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibodies
                                                                                                                                                                                                                                                                       AAT49501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chong P,
               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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                                                                                                                                                                                                                1627 ILCITATTAGGICACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor
                                                                                                                                                                                          142 ICCATAGITITICACGACACITICCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purification of recombinant Haemophilus transferrin-binding protein - by solubilising inclusion bodies separated from cell lysate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and tbp2) under the transcriptional regulation of one promoter. The proteins encoded from these genes can be expressed in a recombinant host., The proteins can be used in vaccines against H. influenzae
                                                                                                                                                                Gaps
                                                                                                                                                                .
0
                                                                                                                                   DB 18; Length 5033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tbpl; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; ds.
                                                                                                                                                                Indels
                                                                                                      Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            H. influenzae strain Eagan transferrin receptor operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein M,
                                                                                                                                                                 0; Mismatches
                                                                                                                                    13.7%; Score 28.2; I
64.6%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harkness R,
Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 4; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAV21429 standard; cDNA; 5033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= Tbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/product= Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0487890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0337483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0175116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0487890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-100410/09.
P-PSDB; AAW53044, AAW53045.
                                                                                                                                                     64.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2165..4903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-1998 (first entry)
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Schryvers A,
                                                                                                                                                                   Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    1687 CATGG 1691
                                                                                                                                                                                                                                                          202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1993;
29-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5708149-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chong P,
                                                                                                                                                                                                                                                                                                                                                                                           AAV21429;
                                                                                   genes.
                                                                                                                                                                                                                                                                                                                                 RESULT 60
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This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae which has antibacterial activity. (I) are used for recombinant production of truncated Tbp; as probe and primers for detecting, and diagnosing infection by, Haemophilus, also for isolating similar sequences from other bacteria; as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g.
                                                                                                                                                                                                                                                                                                                                                            Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                                                                                       1627 Trctrataggicacgaactcccaaggacgacaraccraaaacaggaagrgcaaaaaa 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis, treatment and prevention of bacterial infections, particularly by Haemophilus -
                                                                                                               142 TCCATAGTTTTTCACGACGCCTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                           Gaps
infections or to produce antibodies for use in diagnosis or passive
                                                                                                                                                                                                                                                                                                                                    H. influenzae type B strain Eagan DNA containing Tbp1 and Tbp2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang Y;
                                                                DB 19; Length 5033;
                                                                                           23; Indels
                                      Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schryvers A, Gray-Owen S,
                                                                                             0; Mismatches
                                                                  Score 28.2;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Column 53-64; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Tbp2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Tbp1"
                                                                                                                                                                                                                                                               AAZ89157 standard; DNA; 5033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chong P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0483577.
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93US-0148968.
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P-PSDB; AAY51689, AAY51690.
                                                                     13.7%;
                                                                                   64.6%;
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                            169..2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harkness R,
                                                                                                42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loosmore S, Haram.
                                                                                   Best Local Similarity
                                                                                                                                                                                                    1687 CATGG 1691
                                                                                                                                                                          202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1994;
08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6015688-A.
                      immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2000
                                                                                                                                                                                                                                                                                                                  13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murdin A,
                                                                                                                                                                                                                                                                                            AAZ89157;
                                                                         Query Match
                                                                                                 Matches
                                                                                                                                                                                                                                         RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                       AAZ89157
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 Haemophilus, Neisseria or Branhamella. The truncated proteins are useful
              as immunogens (as above); for diagnosing infection (as antigens in immunoassays) and for raising antibodies, used for diagnosis of infections or for passive immunization. This sequence encodes the transferrin receptor proteins Tbp1 and Tbp2 isolated from H. influenzae
                                                                                                                                                                                                      1627 TICTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies specific for transferrin receptor proteins of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia and tracheobronchitis -
                                                                                                                                                           Gaps
                                                                                                                                                                                   142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial, antiinflammatory, auditory, respiratory, antibody, antiserum, transferrin receptor; immunogen, epitope, otitis media, bacterial meningitis, epiglottitis; pneumonia, tracheobronchitis, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic fragment) from strains of Haemophilus influenzae. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein M;
                                                                                                                                                           .
0
                                                                                                                               Length 5033;
                                                                                                                                                                                                                                                                                                                                                                                                                                 H. influenzae type B strain Eagan transferrin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P, Gray-Owen S, Yang Y,
                                                                                                                                                           Indels
                                                                                                 Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;
                                                                                                                               DB 21;
                                                                                                                                                        23;
                                                                                                                                                       0; Mismatches
                                                                                                                             13.7%; Score 28.2; I 64.6%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Tbp2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Tbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harkness R, Chong
                                                                                                                                                                                                                                                                                                                                             AAZ90999 standard; DNA; 5033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 4; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0148968.
93US-0175116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2165..4903
                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2000 (first entry)
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/product=
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                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schryvers A;
                                                                      type B strain Eagan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-096387/08
                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                        CATGG 1691
                                                                                                                                                                                                                                          202 CCTAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1993;
                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6008326-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1999
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                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                         AAZ90999
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                        1687
                                                                                                                                                                                                                                                                                                                             AAZ90999
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corresponds to the coding sequences for the Tbp1 and Tbp2 transferrin receptor proteins from H. influenzae type B strain Eagan. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottiis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proceins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections.
                                                                                                                                                                                                                                                                                                                1627 TICTIATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
                                                                                                                                                                                                                                                                                      142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutations in nucleic acid molecules encoding 11-cis retinol dehydrogenase correlated to ocular disorders, useful in diagnosis and treatment of diseases such as fundus albipunctatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new protein is described which comprises the 318 residue amino acid sequence corresponding to wild type retinol dehydrogenase (RDH5), but where amino acid 238 is not Gly, amino acid 73 is not Ser, or amino acid 33 is not Ile. This mutant RDH5 can be used in the analysis of
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations in the gene encoding retinol dehydrogenase, in the diagnosis and treatment of ocular diseases associated with retinal degeneration such as fundus albipunctatus. Other disorders which may also be studied include retinitis punctata albescens, albipunctate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-cis retinol dehydrogenase; RDH5; eye; mutant; mutation; ocular disease; fundus albipunctatus; retinitis punctata albescens; albipunctate dystrophy; retinitis pigmentosa; human; ds.
                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                            Length 5033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6330 BP; 1502 A; 1705 C; 1607 G; 1514 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η,
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                       Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto
                                                                                                                                                                                                          13.7%; Score 28.2; DB 21; 64.6%; Pred. No. 36; artive 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-cis retinol dehydrogenase (RDH5) genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berson EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 25-26; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dystrophy and retinitis pigmentosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dryja TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA54431 standard; DNA; 6330 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2000; 2000WO-US12527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0306538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001 (first entry)
                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eriksson U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-016091/02.
                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               1687 CATGG 1691
                                                                                                                                                                                                                                                                                                                                                            202 CCTAG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA54431;
                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                 Matches
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AAA54431/
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                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer \,
                                                             38 CAATITICCAGGACACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGGA 97
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorder, Herpes simplex virus, renal ischaemia; amyotrophic lateral sclerosis; cancer; ds.
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Length 6330;
                                                                                                                                                                                                                                                                                                                                          Chemically treated apoptosis gene complementary to gene #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18683 BP; 6135 A; 130 C; 3515 G; 8903 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78; Indels
                                 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               information supplied by the European patent office.
   DB 22;
                                                                                                                                                                                                                                                                                                                                                                            Apoptosis; HIV; Bloom syndrome; cardiopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                  40;
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   13.7%; Score 28.2; 64.6%; Pred. No. 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Seq ID #34; 24pp; English.
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                                                                                                                                                                                                                                                ABL54334 standard; DNA; 18683 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.77
Best Local Similarity 49.05
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                               29-JUL-2002 (first entry)
                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-017444/02.
                    Best Local Similarity
                                                                                                                                                                  4485 TAAAA 4481
                                                                                                                                    98 TACAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2001.
                                                                                                                                                                                                                                                                                  ABL54334;
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      Query Match
                                     Matches
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2559 igititaaaaatatagtaataataataahtititaaaattataaatatitgatagggaaa 2618

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11 TGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA 70

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2559 İGTİTTAAAAATAİTAĞTAATAATAATAAATİTTAAAATTATAAAATATİGATAGGGAAA 2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTG 130
                                  2619 ATTGAAGAAAAAAAAAAGAAGAAAHGTATTTTGAGTTGAAGATTGGAAAATTA 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
71 ACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA
                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhoumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psortasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 286; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 28.2; D. 49.0%; Pred. No. 59; tive 0; Mismatches
                                                                                                              2679 TTATTAAAATGTTTTTAATATTTAAAGAAATTT 2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                           ABL32313 standard; DNA; 18683
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les 75; Conservative
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                   26-MAR-2002
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                                                                                                                                                                                                                                                 ABL32313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                 131
                                                                                                                                                                          RESULT 65
                                                                                                                                                                                             ABL3231
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invention
                                                    AAX03864;
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                                                                                                                                                                                                                                                                           Colau D,
                                                                                                                                                                                                                                                                                                                                                    vaccines
            RESULT 67
AAX03864/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL22422/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 Terrogacocagoscorogecagosadacacrácicoscoracercacarceacos
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                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 29890.
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                                2679 TTATTAAAATGTTTTTAATATTTAAAGAAATTT 2711
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28;
                     TGACTAACAGGTCCATAGTTTTTCACGACACTT
                                                                                             ВР
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                                                                                          ABL26139 standard; DNA; 726
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Conservative
                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                     26-MAR-2002 (first entry
                                                                                                                                                                                          pharmaceutical; gene; ds.
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                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
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nes 64; Conserv
                                                                                                                                                                                                                                WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 interactions -
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                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                ABL26139;
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                    131
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                                                                        RESULT 66
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method comprises modifying a consensus splicing site in (I). Also described in the present invention are: (1) isolated nucleic acid (Ia) containing a feline calicivirus (FCV) C gene with at least one modified or deleted consensus splicing site; (2) recombinant nucleic acid (II) comprising (Ia) fused to a sequence (III) encoding a polypeptide (IV); (3) vector that can express (I) in the nucleus of eukaryotic cells; and (4) cultures of cells infected with this vector. (II) and the vector of (3) are used in vaccines, specifically to treat or prevent FCV infections. Altering the splicing sites allows coding sequences to be transcribed in the nucleus of eukaryotic cells without alteration by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cells' natural splicing machinery, i.e. without changing the amino acid sequence of the expressed product. The present sequence represents Feline calicivirus strain FCV 2280 capsid gene from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method has been developed for the production of an isolated nucleic acid (I) that can be transcribed naturally in the cytoplasm of eukaryotic cells, without being altered by the splicing machinery. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ATAAGAGGGTTATCACAAAAGCCCAACAGAAAGGAATTTGTTGGGGGTTGACAACTAATCTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing nucleic acid that is transcribed naturally in the cytoplasm of eukaryotic cells - by altering consensus splicing sites, specifically feline calicivirus capsid DNA for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                       Feline calicivirus; FCV; vaccine; capsid gene; infection;
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                                                                                                                                                                                                                                   Feline calicivirus strain FCV 2280 capsid gene.
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AAX03864 standard; DNA; 2007 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 1; 72pp; English.
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                                                                                                                                                       07-APR-1999 (first entry)
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                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 18739.
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0; Mismatches
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11-JUL-2000; 2000US-0614150.
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                                                                                                                               pharmaceutical; gene; ds
                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
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                                                       26-MAR-2002
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3441 rerccascascresassrrcrrsrcsaacresasaaaaasaasrrasccarscrsarr 3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 28; DB 23; Length 3615; 56.5%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2407; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AATTTGGGTGGATTGGCAACAACTTCCTGTG 132
                                                                                                                                      Myers EW;
                                                                                                                                  PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX20669 standard; DNA; 4042
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11-JUL-2000; 2000US-0614150
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                                                                                                                               Adams M,
                                                                                                                                                                                             WPI; 2001-656860/75
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                                                                 (PEKE ) PE CORP NY.
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nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme production;
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                                                                                                                                                                                                                                                                                                                                   interactions -
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                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX20669;
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RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation; diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis; benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
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                                                                       AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3157 CAAAGTTTATTCGGTGGATGATCAGCACGGCATCACCGATCCGCGCAATATCATTGGGGT 3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 CACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 4042 BP; 1035 A; 1216 C; 808 G; 979 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retinoblastoma binding protein-7 genomic DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 39;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
13.6%; Score 28;
Best Local Similarity 55.3%; Pred. No. 3
Matches 52; Conservative 1; Mismatch
Claim 1; Page 833-835; 1150pp; English.
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98US-0111909.
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10-DEC-1998;
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The invention relates to an isolated polynucleotide (ABN27253-ABN31262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therefore.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth \,
                                                                                                                                                                                                                                                                                                                                                                                                            Randazzo F;
                        thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukaemias, and lymphomas. RBP-7 antibodies are useful as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                    33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAA 92
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytostatic; gene expression; gene mapping; tissue profiling; gene therapy; cancer; tumour; gene; ss.
abnormal cell proliferation and/or differentiation, these include
                                                                                                                                                                     Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;
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                                                                                                                                                                                                                                   Score 28; DB 21; Length 162450;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74492 GAGTATCTAATTTAGTAGGTAGGCAGAAAATGTAATTTCTAAAATAG 74539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 CGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAG 140
                                                                                                                                                                                                                                                                                                0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer related polynucleotide SEQ ID NO 3337.
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                                                                                                                                                                                                                                         Query Match 13.6%;
Best Local Similarity 53.7%;
Matches 58; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2000; 2000US-226326P
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DB 24; Length 505;

Sequence 505 BP; 140 A; 130 C; 97 G; 138 T; 0 other;

13.5%; Score 27.8;

Query Match

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The invention relates to isolated polymuciaculus (1) and probes, polymeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of [II]. The and gene mapping, and in recombinant production of [II]. The control of [II] is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cates expressing (II). (I) and (II) are useful in medical cates expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. (II) and polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of the annotations and to produce other types of the invention.

CC amino acid sequences Abs64491-AAS94644 represent novel human continuation ocid sequences of the invention.

CC and partication, but was obtained in electronic format directly from MIPO and in the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed and produce of the invention of the printed an
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                                                               69 GAACAGGATAATAGAACTAAGCAAACGCGATACAATTTGGGTGGATTGGCAAAAAACTTCC 128
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3019 BP; 958 A; 576 C; 649 G; 834 T; 2 other;
                         37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #19678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
ed. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 19678; 103pp; English.
     Pred. No.
                                                                                                                                                                       TGTGACTAACAGGTCCATAGTTTTTCA 155
                                                                                                                                                                                                                    278 rgrgaagaacagaaaaraggrgrrra 252
                                                                                                                                                                                                                                                                                                                                         AAS83874 standard; cDNA; 3019 BP.
                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
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       57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002 (first entry)
                              50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABG19687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                   AAS83874;
                                                                                                                                                                              129
                                     Matches
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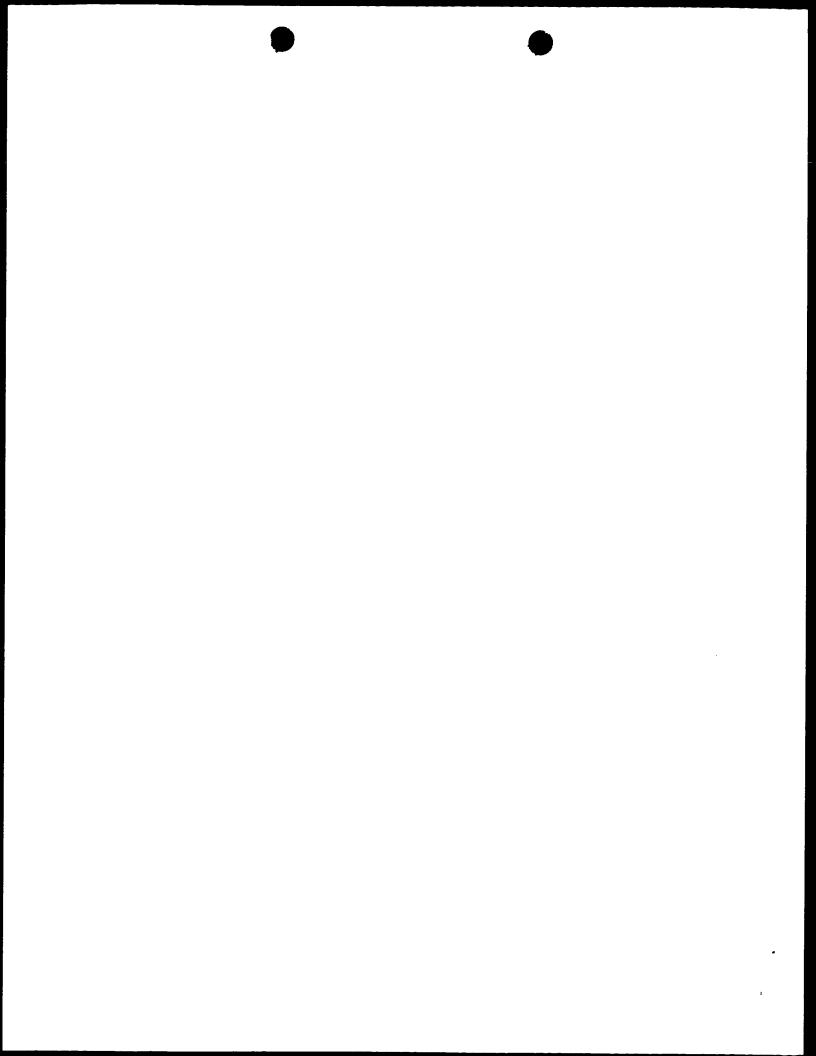
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                    2448 AAGAAAAGACCATAGTATTACCCCATGGGCCAAAATTTTGTCCTATTAGCAAGAATCAT 2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2867 GCCTTAGAGTGGATCTATCGGAGCCCTTGGCCAAGCTCAAGAACTTCGATAAGTCTGTCG 2926
                                                                                                                                    67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTT 126
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 39119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Length 3019;
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                                                                   Indels
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DB 23;
                                                                   27;
13.5%; Score 27.8; DE 62.0%; Pred. No. 41; Live 0; Mismatches
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11-JUL-2000; 2000US-0614150.
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                                Best Local Similarity 62.0
Matches 44; Conservative
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Matches 44; Conserv
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   Query Match
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ABL14879
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Oy 67 AAGAACAGGAT 77

Db 2927 AGAAACTTAAT 2937
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Search completed: February 15, 2003, 22:38:28 Job time : 1488 secs



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February 15, 2003, 21:53:32; Search time 1184 Seconds (without alignments) 2817.796 Million cell updates/sec
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1 gctcgagccatggtatggac......gcaaggtgttattatcctag 206
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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7348 LMCROSOO 8639 AGENCOUR 8377 CM1-CIOO 1181 Drosophi 67713 wv44alp 1738 nz10b01 738 nz10b01 8686 EST38076 4905 50072-2- 44605 fc1127.e	4449 ENIDY59T 1315 AG-ND-15 3526 RPCI-23- 0124 Anophele 1214 Anophele 1219 BOGMO80T 1219 ALS 2214 8884 ZMC1280 8855 AU00585 8329 C006H03 4945 CMC4610 4945 CMC4610	1479 ENICASZI 17018 AGENCOUR 18766 CIT-HSP- 18766 CIT-HSP- 1875 BOGTD72T 1875 BOGTD72T 1875 BOGTD72T 1875 BOGTD72T 1876 BOGTD72T 1876 BOGTD72T 1876 BOGTD72T 1877 BOGTD72T 1877 BOGTD72T 1877 BOGTD78	30330 CM130 CM130 SMC13 SMC13 SMC17
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AQ963598 603 bp DNA linear GSS 28-JAN-2000
LERGM96TRC LERG Arabidopsis thaliana genomic clone LERGM96, DNA
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/strain="Landsberg erecta"
/db_xref="Laxon:3702"
/clone="LERGM96"
/clone="LERGM96"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 116 9 207 t
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T3 end of clone AVOAA005E04 of library AVOAA from strain CBS 379 of
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1 (bases 1 to 603)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Geldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 401 838 0208
Fax: 401 838 0208
For additional information, see http://www.tigr.org/tdb/at/at.html
261 GACTCATTATATGATCACATATAAGAACAAAGGTGTGTGCCGCATCATATAGCCTATGGT 320
                                                                  321 TCGAGATCAAAACTAATCCACTAAGCTTCAAGACTAAAACTTACATCTGTTGGCAACCAAT 380
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                                                                                                   125 TTCCTGTGACTAACAGGTCCATAGTTTTTC 154
                                                                                                                                    381 CTACTCTATGTAACAGGTTTCTAGTATTGC 410
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Unpublished (2000)
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BIO66490 D97111.DR0
B99323 CIT-HSP-228
BM958613 PLATE 9 C
BF187411 EST443698
BM95868 PLATE 11
BF711054 MI-P-AX1
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BM958781 PLATE 10
BM958897 PLATE 18
AQ170967 HS 2197 A
BE603939 GSZ56 GS
BE603771 GS212 GS
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/note="Organ: Leaf, Vector: pUC19JK, Total genomic DNA was
sheared to 0.4-0.7 Kbp before ligation."
118 c 137 g 149 t
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 604)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyuw, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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BM959198 PLATE 11
AV827484 AV827484
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For addtional information, see http://www.tigr.org/tdb/at/at.html
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LERGM96TF LERG Arabidopsis thaliana genomic clone LERGM96, DNA
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Unpublished (2000)
Conteact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
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/db_xref="taxon:3702"
/clone="LERGM96"
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                AQ591379
BI065490
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AQ963597.1 GI:6791282
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Best Local Similarity 53.34
Matches 80; Conservative
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Class: shotgun.
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Submitted (22.406-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Core eudicots; Core eudicots; Asteridae, euaterida I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 721)

1 (bases 1 to 721)

1 (bases 1 to 721)

1 (bases 2 to 721)

1 (bases 3 to 721)

1 (bases 4 to 721)

1 (bases 5 to 721)

1 (bases 6 to 721)

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1 (bases 1 to 721)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998)
2 (bases 1 to 721)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
                                                                                AG012919 721 bp DNA linear GSS 08-FEB Homo sapiens genomic DNA, 21q region, clone: f1E12X11, genomic
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073H05 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA
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Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 t
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Location/Qualifiers
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/chromosome="21"
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173 c 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 ENRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr. web: www.genoscope.cns.fr. (E-mail: seqref@genoscope.cns.fr.) rhis GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum Saccharomyces exiguus, Saccharomyces servazzil: Zygoasccharomyces ouxii, Saccharomyces Rluyveromyces thermotolerans, Kluyveromyces tactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lanssenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                           Saccharomyces exiguus.
Saccharomyces exiguus
Saccharomyces exiguus
Saccharomycetales, Fungi, Ascomycota; Saccharomycetus; Fungi, Ascomycota; Saccharomyceteles;
Saccharomycetales; Saccharomycetacee; Saccharomyces.

1 (bases 1 to 852)
Society.J.L., Aigle, M., Ariguenave, F., Blandin, G.,
Souciety.J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

L. FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to Saccharomyces cerevisiae ORF YBR068c [BAP2 ; leucine permease, high-affinity (S1) ] similar to Saccharomyces cerevisiae ORF YDR046c [BAP3 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bon, E., Neuveglise, C., Lepingle, A., Wincker, P., Artiguenave, F., Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        727 ACACAGTITATIGAAICTIAAAATAAACTIAIATAAAGTAACCAACGTGACATTITCCATA 786
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Saccharomyces exiguus, genomic survey sequence.
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/clone="AV0AA005E04"
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/note="end : T3"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
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/clone=hqg2c05"
/clone lib="mqgs.zmaysF (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH874885 63 bp DNA linear GSS 05-AUG-hq82c05.gl WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hq82c05 5', DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katzenburger, F.D. (O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McComble, W.R. and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Loid Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 GGAGGAACATCAGTTGCCAGGGAAATTTCAGTAGTAGTGTCAATGCATAACGGAACAGGA
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                                                                                                                                                                                                                                                                                                                         16.3%; Score 33.6; DB 12; Length 721; 52.1%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                     69; Indels
                                                                                                                                              /cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
                                                                                                                            /organism="Solanum tuberosum"
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                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/note="Vector: Lambda ZAP"
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Location/Qualifiers
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Plate: hq82 row: c column: 05
Seq primer: -21M13UnivFwd
                Email: kgw@bio.auc.dk
High quality sequence stop: 721
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                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.19 tes 75; Conservative
Fax: +45 98141808
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was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
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Methyl-filtration library, Nuclei DNA was completely
digested with Mcr BC, size fractionated and transformed
to E.Coli.DH10B. 174 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMCR050012H06f Zea mays L. Zea mays genomic clone LMCR050012H06f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 AATTCAACATTACACCACATTATCTACAATCAATGGTTACTGGAATAAAGATGAGAAG 322
                                                                                                                                                                                                                                                                                                                                          51 ACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 ATTICCAGGACACAGATGGTTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATA 99
                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               132 ACACCATÁTTATCTACAATCAATGGTTACTGGAATAAAGATGAGAGAAGCATTTTGGGTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 33.2; DB 17; Length 607; 57.8%; Pred. No. 8.5;
                                                                                                                                                                                                                                 16.2%; Score 33.4; DB 17; Length 663; 60.4%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 607)

Kim,S.W., Yu,Y., Lee,W.C., Main,D. and Wing,R.A.

Methyl-filtration genomic sequence from maize

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                        0; Mismatches
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/clone="LMCR05012H06f"

/clone_lib="Zea mays L."

/tissue_type="Leaf"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 GATTGGCAACAAACTTCCTGTGACTAACAGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Total High Quality bases = 546
Seq primer: TAATACGACTCACTATAGGG
Class: shotgun
High quality sequence start: 2
High quality sequence stop: 598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 TATAGGTGACAAACATAATGCAACAATCAGG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     607 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH837348.1 GI:21235226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="B73"
                                                                                                                                                                                                                                                                                        55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence.
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICAGGAAAIGGCITITITAGGAGITITITACIGA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL071181.1 GI:4951021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 51.0°
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .298
                                                                                                                                                                                                               Simpson, A.J.
                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Brazil
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ORIGIN
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SOURCE
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                                                                                                     AUTHORS
                                                                                 REFERENCE
                                                                                                                                                                                                                                                                               JOURNAL
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SOURCE
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                                                                                                                                                                     BM458639 1292 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6413495 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497704
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1292)
MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library." 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.e column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 TGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 GGCCTAAAAAGCCACAAATGTTGCCCAGACCTTTTAAAAAACCCACTCATAACAAAGGAA 371
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 1292
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5497704"
/clone=lib="WIH MGC 85"
/lissue type="lymphoma, cell line"
/lab_hogt="DH10B (phage-resistant)"
                  100 CAATTIGGGIGGATIGGCAACAACTICCIGIGACIAACAGG 141
                                                          323 carrirgegrariagergacaacaacaraargcaacaarcaag 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                        BM458639.1 GI:18507679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF818377.1 GI:12155643
                                                                                                                                                                                                      5', mRNA sequence.
BM458639
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                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                     human.
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ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
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                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
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                                                                                                                          RESULT 8
BM458639
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/organism="Homo sapiens"
/db xref="taxon:966"
/clon=lib="c10032"
/dev stage="Adult"
/note="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI, A minI-library was made by cloning products
Site_2: SmaI, A minI-library was made by cloning products
derived from Organs PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR31K23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 298)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=CM1&t2=CM1-CI0032-19100-630-cl1&t2=2000-12-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence start: 298.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 Arcrerecrerasasecreseserriciesesaseareresesasecasareserens 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 Trcrrrcegeaheregeaacraaeccareaeacaacraaeccarcrceaeaacaacr 81
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0
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2460 Std Error: 0.00
Seq primer: -400P from Gloco
High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA760738 467 bp mRNA linear EST 18-FEB-1998 nz10b01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287337 3',
                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: stomach, Vector: pCMV-SPORT6; Site 1: Sall; Ste 2: Not!; Cloned unidirectionally. Primer: Öligo dT. Average insert size 1.69 kb. Life Technologies catalog #:(11549-011")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 467)
                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:2532378"
/clone lib="NCI CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACCTAACAGGTAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 ACGIATACGAGITCTIGGICAATTICCAGGACACAGAIGAITCGGICCAAGAACAGGAIA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2366 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 466.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 CTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 33; DB 17; Length 1101; 43.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:7227"
/clone="BACR31K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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  Drosophila melanogaster
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Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" 88 c 166 g 170 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
TTE: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .633
/organism="Gossypium arboreum"
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Clemson University Genomics Institute
                                                                                                        Score 32.6; DE
Pred. No. 13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   159 CACTTCCAAGGACGCCATACCGAACAAAGCA 189
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Total High Quality bases = 114
Seg primer: TAATGGACTCACTATAGGG
High quality sequence start: 52
High quality sequence story: 569.
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                                          166 g
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BQ413342.1 GI:21101029
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                                                                                                          15.8%;
51.0%;
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                                                                                                                                                  77; Conservative
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                                                                           ). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,
C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from comato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="callus"
/dev stage="25-40 days old"
/dab_host="XL1-Blue MRF"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607 bp mRNA linear EST 18-MAY-20 EST274620 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC34H22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 383
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                             ch 15.8%; Score 32.6; DB 9; Length 467; 1 Similarity 57.3%; Pred. No. 12; 59; Conservative 0; Mismatches 44; Indels (
                 /clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato callus, TAMU"
  /clone="IMAGE:1287337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC34H22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GA_Ed0073B06r Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ed0073B06r, mRNA sequence.
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                         177 TCTGTTGAGCTGCATTGTCAACATCATATCTATACTAACCACATTTTCACCTTCTT 118
                                                                                                                                                                                                                                 237 AGTATCTGGGCCCCCCGAAGAGCCTTCGTAGGACGACACCATTAGACATATCAACGGGAT 178
                                                                                                                                                                                                                                                                                                         99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGA 158
                                                                            0; Gaps
                                                                                                                                                        39 AATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGAT 98
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133 c 130 g 191 t 22 others
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DB 10; Length 607;
                                                                        74; Indels
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BQ104605.1 GI:20154267
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Rosa hybrid cultivar
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                                                                                                                                                                                                                                                                                                                                                                                              86; Conservative
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 1351)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
'J. and Klobutcher,L.
Eng from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 699)
Hegde, P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
.1.B. Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
                                                                                                                                                                                       EST380762 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                          Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 3528
192 AGTICATINITCATITCCAGGACAAAATGAATCGTTAAGAACACAGATTAAGAAATTA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 371
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                                                                                                                                                                                                                                                                                                                      Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db.xref="taxon:9606"
/clone_lib="wAGE resequences, MAGJ"
/note="Vector: pBluescriptSKm"
142 c 107 g 224 t
                                                                                                                                                                      mRNA
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Plate: 256
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                                     88 AGCA 91
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BQ104605 502 bp mRNA linear EST 16-APR-2002 fc1127.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library Rosa hybrid cultivar cDNA clone fc1127.e 5', mRNA sequence.
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Chilcoat/Turkewitz SK+, Details on library
/note="Vector: Bluescriptz SK+, Details on library
/preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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1 (bases 1 to 502)

Menda,N., Guterman I., Piestun,D., Emanuel,M., Adam,Z., Pichersky E., Lewinsohn,E., Zamir,D., Vainstein,A. and Weiss,D.

Rose petal genomics: an integrated approach to discover
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730 TATTAGCCAAAAACAGGGGGGGGGGGGGGGGTTAAACCCACGGCGAATCGGAAGGGGC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AACGCGATACAATTTGGCTGGATTGGCAACAACATTCCTGTGACTAACAGGTCCATAGTT 150
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/clone="fc1127.e"
/clone="fc1127.e"
/clone=libe="fc1127.e"
/clone=libe="fc186756"
/tissue_type="Petals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TITCACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTATCCTA 205
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    1351
/organism="Tetrahymena thermophila"

                         University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
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Molecular Genetics and Cell Biology
                                                                                              rel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: 73
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Seg primer: T3 forward.
Location/Qualifiers
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCR-Script; Total genomic DNA was nebulized; ends were polished with Pfu polymerase and the fragments cloned into pCR-Script."
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Meyers, B.C., Tingey, S.V. and Morgante, M.
Meyers in the maize genome
Genome Res. 11 (10), 1660-1676 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Maize Random Small-insert Genomic_Library"
/sex="hermaphrodite"
                                                                                                                                                           92 ACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTT 151
                                                                                                                                                                                             49 ACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AGACACCATATTATTACAAGCACAGCTACTGGAATAAAGATGAGGAGCATTTTGGA 194
                                                                                                                            Gaps
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/dev_stage="Young open flower at stage four"
/note="Vector: pBKCMV, Site_1: EcoRI; Site_2: XhoI"
144 c 117 g 114 t
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                                                                                       Score 32.4; DB 14; Length 502;
Pred. No. 14;
0; Mismatches 46; Indels 0
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                                                                                                                                                                                                                              152 TTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
                                                                                                                                                                                                                                                               270 chartgaaaccccaaggacarcartargcagrcrgcaaggccha 315
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59.1%; Pred. No. 14;
tive 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 6104, Newark, DE 19714-6104, USA Tel: 302 631 2638
Fax: 302 631 2607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaf"
/cell_type="Young leaf"
/dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="B73"
/db_xref="taxon:4577"
/clone="G-4m17"
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                                                                                         15.7%;
56.6%;
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Class: shotgun.
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                                                                                                                          60; Conservative
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Email: szhoo@tigg.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/bacpac/or ering_information.htm). BAC end
Plate: 81 row: C column: 23
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                                                                                                                                                                                                      BH349323 TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-81C23, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 198)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
Zhao, S., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., d
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: Eco
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 CAGAATCTAAGACTACCAGGCATCTTCAGAGCACAGTACTCCAAAACCAAAGCAAGTTGTGG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10116"
/clone="CH230-81C23"
/clone lib="CHORI-230 Segment
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
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      141
                                                       195 CATATAGGTAACAAGATGCAACAATCAGG 227
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Department of Eukaryotic Genomics
109 TGGATTGGCAACAACTTCCTGTGACTAACAGG
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                                                                                                                                                                                                                                                                                                                          BH349323.1 GI:17280057
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Class: BAC ends.
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /d_arel= "Entamoba histolytica Sheared DNA"
//d_arel= "Entamoba histolytica Sheared DNA"
//doce="Vector: pHOS1; Site_1: Bst 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, Ho. and Venter, JC. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG-ND-157F23.TF ND-TAM Anopheles gambiae genomic clone AG-ND-157F23.
, DNA sequence.
BH387315
                                                          AZ54449 865 bp DNA linear GSS 14-NOV-2000 ENTDY59TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                              Bukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 865)
Loftus, Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17; Length 865;
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                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 24;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 17
High quality sequence stop: 818.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13-Reverse
Class: shotgun
                                                                                                                                           AZ544449.1 GI:11164297
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                                                                                                                                                                                      Entamoeba histolytica.
Entamoeba histolytica
                                                                                                      genomic, DNA sequence.
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Best Local Similarity 55.4%
                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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BH387315
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TITLE
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Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 03543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is Gerived from mixed sexes of larvae. The BAC
library was constructed at Texas ARM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 450)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardnez,M. and Loftus,B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
Other GSSS: AG-ND-135F11.TR
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG-ND-135F11.TF ND-TAM Anopheles gambiae genomic clone AG-ND-135F11 , DNA sequence.
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                                                                                                                                                         Gardner, M. and Loftus, B.J.
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                                                                                        Anopheles.

1 (bases 1 to 421)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus
Direct submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
Other_GSSS: AG-ND-157F23.TR
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/note="Vector: pECBAC1; Site_1: HindIII"
77 c 88 g 131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 31.8; DB 17; 57.6%; Pred. No. 20;
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The Institute for Genomic Research
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/clone="AG-ND-157F23"
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                                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
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Seq primer: M13 For
Class: BAC ends.
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BASE COUNT
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KEYWORDS
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                                                                                      This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: sthatography org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library and albility, please contact Piecer de Jong
Ibrary availability, please contact Piecer de Jong
(piecer@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.8; DB 17; Length 450; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 bp DNA linear GK
RPCI-23-270F11.TJB RPCI-23 Mus musculus genomic clone
RPCI-33-270F11, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:7165"
/clone="AG-ND-135F11"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
80 c 93 g 144 t
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 TCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 ACCAAAGATGCATAATCAAACATGCAAATGGATTAATAT 350
                                                                                                                                                                                                                                                                                                                                                                                        1. .450
/organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                       Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="PEST"
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57.6%;
                                                                                                                                                                                                                                                                                       partial digest.
Seg primer: M13 For
Class: BAC ends.
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Best Local Similarity
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JOURNAL
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//sex="Female"
/lab host="DH10B"
/lab host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
bcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomIc DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
a 107 c 102 g 112 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVR7 cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Chases 1 to 617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CCAAGAGGAATAAAACAAAACTAAAACAACAGAACTAATGTTGGATGAATGCCATCATGC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31.8; DB 17; Length 512;
Pred. No. 22;
0; Mismatches 42; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 crccagcracaacccagcccarcraaarrcaaracacar 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 TTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .617
/organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u
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                                                    organism="Mus musculus"
                                                                                                       /db xref="taxon:10090"
/clone="RPCI-23-270F11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NotreDamel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:7165"
/clone="22F09"
                                                                                                                                                              /clone lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="end : SP6"
104 c 118 g
Location/Qualifiers
                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence. AL610124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL610124.1 GI:15916309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%;
57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles.
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ALS52214 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1069YA02 3
                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 590)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="BOGW"
/note="Vector: pHOS1, Site 1: BstX1, 2-3 kb sheared
genomic DNA inserted into pHOS1 using EstXI linkers"
1 138 c 120 g 253 t
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BP 191 91006 BVRX cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 684;
                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
                                                                                                                                                                                        Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 31.8; 53.7%; Pred. No. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3712"
/clone="BOGWO80"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                        BH521915.1 GI:17730000
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Contact: Chris Town
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AL552214
                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: sheared ends
                                                                                                                                                                         (bases 1 to 684)
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                                                                 Brassica oleracea.
                                                                                       Brassica oleracea
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    BH521915
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                                                                                     ORGANISM
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ORGANISM
                                                                                                                                                                         REFERENCE
AUTHORS
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JOURNAL
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  ACCESSION
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                                           KEYWORDS
SOURCE
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                               103 TITIGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACT 162
                                                                                                       65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
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                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="TO10000DH3"
/db xref="taxon:3712"
/clone="BOGG1144"
/clone_lib="BOGL"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
a 125 c 123 g 234 t
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                                                                                                                                                                                                                                                                                                                   BOGLI44TR BOGL Brassica oleracea genomic clone BOGLI44, DNA
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BH521915
BOGWO80TR BOGW Brassica oleracea genomic clone BOGWO80, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGLI44TF
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                        42; Indels
                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                        307 ACCAAAGATGCATAATCAAACATGCAAATGGATTAATAT 345
                                                                                                                                                 163 TCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
57.6%; Pred. No. 24; ive 0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                  648 bp
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                        57; Conservative
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301-838-0208
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  Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            sequence.
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BH513269/c
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BH521915/c
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TITLE
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COMMENT
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musculus C57BL/6U/female) was obtained from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically should be constant velocity. The sheared DNA was but end are repaired with TA DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalpat (gil #732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                             251 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 15.3%; Score 31.6; D. Similarity 55.5%; Pred. No. 29; 61; Conservative 0; Mismatches
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51.0%; Pred. No. 38;
tive 0; Mismatches
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/db_xref="taxon:7091"
/clone="wv40184"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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2M0212B07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0212B07 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 ATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACT 135
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/clone="UUGC2M0212B07"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.3%; Score 31.6; DB 9; Length 590; Best Local Similarity 54.2%; Pred. No. 27; Matches 52; Conservative 5; Mismatches 39; Indels (
                                                                                                                                                                                                                                                                                                                                       54 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: B column: 07
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 653.
Location/Qualifiers
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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organism="Homo sapiens"
                         /db xref="taxon:9606"
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1 (bases I to 852)

Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Establishment of cDNA database of Bombyx mori
Unpublished (1999)
                                                                                                                17 GGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGA 76
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                                                                                                                                                                                                                                                                                                   540 AAATTAAAGTAACTTACTCTATCCAATCTGATTAAAATGGAATTAAAGTT 491
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                                                        49; Indels
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National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmitae@nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
DB 17;
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Query Match
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
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Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu
H.F., Jiang, Y.X., Yu, F.C., Gao, O.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="C006H03"
/clone_lib="Oryza sativa mature leaf library induced by
109 TGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAG 168
                                                                                           663 TATAGTTCGAAGAACCTTGTTGAGAGTGAACTGAGTCTAATCTTCCACAACATTAGCAAC 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
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/note="Vector: pSport2"
102 c 105 g 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
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                                                                                                                               169 GACGCCATACCGAACAAGCAAGGT 193
                                                                                                                                                                    603 TGCATCAAGCGCATCAGAAAAGAT 579
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/note_notering pryral-Pac; Site 1: EcoRI; Site 2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pryral-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Researc 6:791-806, 1996. The first strand synthesis used a NotI-dr18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pryral-Pac vector. The library contained approximately 7:2 X 10°5 recombinants, with average insert sizes of 1-1:5 kb."
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Kenpibia, Kanopus.

1 (bases 1 to 636)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
first 13,879 ESTS from unfertilized eggs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Barkway, Huntsville, AL 35901
phone 800-53344363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
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/db xref="taxon:815s"
/clone="PR0146c01"
/clone=lib="Blackshear/Soares normalized Xenopus egg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Seg primer: T7 primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 919 541-4899
Fax: 919 541-4571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .636
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RESULT 32 AZ858033/c

AW644945.1 GI:7402350 EST. African clawed frog.

ACCESSION VERSION KEYWORDS SOURCE

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/db xref="taxon:7165"
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                                                                                                                                                                                                                                                                                                                 African malaria mosquito.
                                                                                                                                                                                                                        , DNA sequence.
BH381988
BH381988.1 GI:17328130
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AZ684794
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Class: BAC ends.
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                         204
                                                                 177 TTTTAATGCCTT 166
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Best Local Similarity
                       193 TGTTATTATCCT
                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles.
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                                                                                                                                   RESULT 33
BH381988/c
                                                                                                                                                                                                   DEFINITION
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ858033 658 bp DNA linear GSS 21-FEB-2001 2M0163L02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0163L02 F, DNA sequence.
                                                                                                                                                      Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 658)
                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-" /note="Vector: PM742nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 AGGAAGTTTGAAGTTGGCCTCACTAATTTACATAGGTGGCTTAGACAAACTCTTCAACTT 238
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/clone="UUGC2M0163L02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: L column: 02
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 658.
Location/Qualifiers
                                                                                       AZ858033.1 GI:13050772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 03543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas ARW Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          872 bp DNA linear GSS 14-DEC-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
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BH381988 801 bp DNA linear GSS 10-DEC-2001
AG-ND-172E18.TR ND-TAM Anopheles gambiae genomic clone AG-ND-172E18
                                                                                                                                                                                                                                                                                                                                                                           Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other GSSs: AG-ND-172E18.TF
Contact: Brendan J Loftus
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                                                                                                                                                                                                                                              Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/clone lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
216 c 157 g 280 t
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/db xref="max.ning" | /db xref="max.ning" | /db xref="max.ning" | /db xref="wettor: pHOS1; Site=1: BRE 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamocba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kD). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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5', mRNA sequence.
                                                                                                                                                                                                                                                                                  Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seg primer: M13-Reverse
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library (2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACATCCTGTGAC 134
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 888;
                                                                                               Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
7712 Mod 38 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Entamoeba histolytica"
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53.2%; Pred. No. 45;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 25
High quality sequence stop: 807.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="HM1:IMSS"
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/db_xref="http://db.
/db.xref="http://db.
/dlone lib="Entamoeba histolytica Sheared DNA"
/note="wector: ph0S1; Site=1: BSt J; Constructed at The
Institute for Genomic Research (FIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     888 bp DNA linear GSS 27-AUG-2001
ENTPD89TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
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                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Fax: 301 838 3543
Elamil: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
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Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                          Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 ATAGICTTATAGCAGTTTTACTTGGATTAACATTACAATCAATTTCTTTATTAACAT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%; Score 31.2; DB 17; Length 872; 53.2%; Pred. No. 44;
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0; Mismatches
                                                                                 Eukaryota; Entamoebidae; Entamoeba.
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 888)
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Class: shotgun
High quality sequence start: 127
High quality sequence stop: 823.
Location/Qualifiers
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                                                                                                          (bases 1 to 872)
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                                                                                                                                  AUTHORS
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                                                                                                                                                           TITLE
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/db_xref="taxon:4530'
                                                Location/Qualifiers
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AQ257960.1 GI:3782442
                                                                                                                                                                                                                                                                                                                                                     15.0%;
56.3%;
                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                   159 c
  Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                      HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   58;
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                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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COMMENT
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                                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                              /clone libe NIH MGC 47"
/tissue type="neuroblastoma, cell line"
/labhost="BH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site 1: Xho1; Site_2:
BcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5'
adaptor: GGCACGAG(G). Size-selected 500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library.

10 thers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished GSSs: CIT-HSP-2367F1.TR
Other GSSs: CIT-HSP-2367F1.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 580)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Barry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIT-HSP-2367F1.TF CIT-HSP Homo sapiens genomic clone 2367F1, DNA
                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM5562 row: 1 column: 17
High quality sequence stop: 514.
Location/Qualifiers
1. 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.1%; Score 31.2; DB 14; Length 9 Best Local Similarity 57.0%; Pred. No. 46; Matches 57; Conservative 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 CAAAAATTTAAAATGGAAATAAAAAATTCAAACAAATT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6378016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 bp
Email: cgapbs-r@mail.nih.gov
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AQ078766
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KEYWORDS
SOURCE
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608 bp DNA linear GSS 23-OCT-1998 nbxb0019B15r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019B15r, DNA sequence.
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world popularion especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohytrate. Monocovyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 411 Mbp
(Arumuganathan and Earle, 1991). The relatively small
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Coryza sariva

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

I (bases 1 to 608)

Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 TCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCG 96
                                                                                                                                                                        /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                              Score 31; DB 17; Length 580; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 AGTAACTTTCCTTTAAAGGGCTCCAAACCTCCTGCTACCAAAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
11 Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
1. 580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2367F1"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 424.
Location/Qualifiers
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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123 ACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAA 182
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Location/Qualifiers
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                                                                                                           183 CAAAGCAAGGTGTTATTATCCTA 205
                                                                                                                                                   649 AATCAGTGTTTGTTGTTTCTTA 671
                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                  AL697315.1 GI:19616789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Kafatos, F.C.
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JOURNAL
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genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryas sativa, Nippombare variety. The library contains 36.864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH461787 BOGT Brassica oleracea genomic clone BOGTD72, DNA BOGT BOGTD72, DNA
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Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales; Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAA 122
                                                                                                                                                                                                                                                                                                                                                                     42 TTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 TTACAGTGGGGAAAGCGTAAGGCAAAACAACTAGAATTGACCTACATTACGCATAAAA 334
                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
                                                                                                                                                                                                                                                                                     15.0%; Score 31; DB 17; Length 608; 56.3%; Pred. No. 43; tive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 17; Length 873;
Pred. No. 51;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 ATTIGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 ATATAGGITGCATAATAACAAATCTCTGCTACTAATCGCTCC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3712"
/clone="BOGTD72"
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BH461787.1 GI:17652271
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51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                  Conservative
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301-838-0208
                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                          Query Match
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ORGANISM
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TITLE
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/clone_lib="NAP1"
/lab host=""B. APP1"
/lab host="E. Coli DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia); Site_l: NotI;
Site_2: ECORI; ESTS sequenced from the T7 priming site
that reads from the 5' end of cDNA. The NAP1 is a
directionally cloned and normalized, oligo-T primed cDNA
library constructed from a mixture of Anopheles gambiae
developmental stages according to: Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
6, 791-806."
                                                                                                                                                                                                                                                                                                                                 AL697315 AAC97315 AAC97315 NAP1 Anopheles gambiae CDNA clone NAP1-P54-D-02-5, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1749 MMKDRVÄCAMRKABÄKWYRGGÄGÄKCASRCCBARGCRBANMÄNRMNMKNTNDGAKMMKVG 1808
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589 ATTITGIGIGATGATTGITGCCGACATATTCGGGATTCATCCAACGAACCAATACAGAA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 AATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACAACTTCCTGTGACTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae EST, European Molecular Biology Laboratory Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Christophides GK
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
Far: +49 6221 387-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Anopheles gambiae"
/db_xref="taxon:7165"
/clone="NAP1-P54-D-02-5"
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University of Minnesota
1988 Fitch Avenue, University of Minnesota, St. Paul, MN 55108, USA
TTE1: 612 624 1246
Fax: 612 625 0204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Brain; Vector: pSPORT1 (Gibco BRL); Site_1: Mot1; Site_2: Sall; Tissue was taken from the frontal, occipital, temporal and parietal lobes, olfactory bulb, hippocampus, cerebellum, thalamus, hypothalamus, midbrair hippocampus,
                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 581)
                                                                                               Roberts, M.C., Handrickson, J.A., Hoffmann, D.E., Flickinger, G.H., Rutherford, M.S. and Mickelson, J.R.
University of Minnesota Canine Brain EST Project
Unpublished (2001)
Contact: Mickelson, J.R.
Veterinary Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 Grarccaagriccrgarggaarrcrggricagaacacrcgaracaagcarrngcaaa 414
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                                                                                                                                                                                                                                                                                                                                                                                               /organism="Canis familiaris"
/db_xref="taxon:9615"
/clone_lib="Canine Brain cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
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/db_xref="taxon:31033"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.8; D
Pred. No. 49;
0; Mismatches
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186 c 172 a
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Takifugu rubripes.
Takifugu rubripes
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                                                                                                                                                                                                                                                                                                               Email: micke001@umn.edu
Seg primer: M13 Reverse
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AL015113.1 GI:2681481
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58.8%;
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  dog.
Canis familiaris
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Best Local Similarity
Matches 50; Conserv
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COMMENT
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FR0022243
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VERSION
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                                                                                                                                                                                                                                                                                  Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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                                                                                                                                                                                                                              1 (bases 1 to 427)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.
                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see
                                                                                                                                                                                                                                                                                                                                                                                             Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.insc.nih.gov.

This clone is available royalty-free through LiNL; contact the

This clone is available royalty-free through LiNL; contact the

TMAGE Consortium (info@image.llhl.gov) for further information.

Plate: LiAM6191 row. L column: 24

Seg primer: M13RP1 reverse primer (ABI).
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0; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ccmorton@bics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.8;
Pred. No. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                              Contact: Morton, C. C.
                                                                                                    AW024040.1 GI:5877570
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l Similarity 54.4%;
62; Conservative
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Best Local Similarity
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                                                                                                                                                                 ORGANISM
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COMMENT
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AW024040
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midbrain

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Gaps

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Length 581;

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FR0022243 416 bp DNA linear GSS 10-DEC-1997 F.rubripes GSS sequence, clone 074I20aF3, genomic survey sequence.
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1 (bases 1 to 416)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk vector: pBluescript II KS V type: pBluescript PR V PyPe: PApagemid PR V FYPE: KS
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DEFINITION
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                                                                                                              KEYWORDS
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priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                           AW264970 458 bp mRNA linear EST 28-DEC-1999 xq58f08.x1 NCI_CGAP_Co22 Homo sapiens cDNA clone IMAGE:2754855 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                           192 AGCTCTTTGCCANTTTAAAAACCCGGAATTTTAAGTNAAAAAATTNGTCAAAACCACTA 251
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                                                                                                                                  0; Gaps
                                                                                                                                                                     28 AGTICTIGGICAATITICCAGGACACAGAIGAITICGGICCAAGAACAGGAIAAIAGAACIA 87
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0; Mismatches 34; Indels
                                     25 others
                                                                                                                                50; Indels
                                                                                                                                                                                                                                                                                  252 ACACAANTGCTATAAAATGGGGGGAAANTNAAAAACTAGCAGGGTC 298
                                                                                                                                                                                                                                                88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGS:754685s"
/clone=lib="NCI_CGAP_Co22"
/tissue_type="colonic adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown library type
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
                                     106 t
                                                                                                              Pred. No. 48;
0; Mismatches
                 /clone_lib="cosmid 074120"
78 c 61 g 106
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                                                                                          Score 30.6;
Pred. No. 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                   61 9
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/clone="074I20aF3"
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                                                                                                                              57; Conservative
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AZ900700 539 bp DNA linear GSS 05-MAR-2001
RPCI-24-173H24.TV RPCI-24 Mus musculus genomic clone RPCI-24-173H24
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Mouse BAC End Sequences from Library RPCI-24
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Clones are derived from the mouse BAC library RPCI-24. For BAC
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/organism="Mus musculus"
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/clone="RPCI-24-173H24"
/clone_lib="RPCI-24"
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KEYWORDS
SOURCE
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N65641 Lambda-PRL2 Arabidopsis thaliana cDNA clone 240K9T7, mRNA
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Viridiplantae, Streptophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 304)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM899 row: g column: 07
High quality sequence stop: 596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 69;
                                                                                                                                       /organism="Homo sapiens"
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Fax: 517-353-9168
Emall: 22313tcn@ibm.cl.msu.edu
Seg primer: T7 dye primer.
                                                                                           Location/Qualifiers
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51.9%;
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Best Local Similarity
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N65641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: DBluescript SK(-); Site 1: BcoR1; Site 2: Xho1; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tubers, or roots."
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                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum.
I (bases I to 720)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
                                                                                                                                                                                                                                                                                                                            Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues" //tissues-type="mixed tissues" /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 862)
1 thrus-(hufp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                       Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)
Other ESTs: EST621795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement. ATCC
CDN Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618 AGCTCTAGGGCTACTTCGAGGGTCCATAGTAGGGGATGAGTTGACAGAAAAAGAGAAGA 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.9%; Score 30.6; DB 14; Length 720;
Local Similarity 56.4%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Indels
                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 AGCATTGCGGAGAACTTTTACTGACTTGGCATCAGTCGTAC 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMIL58"
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/organism="Solanum tuberosum"
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BF185163.1 GI:11063592
                                                                                                                                                                                                                                                             Contact: Robin Buell
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       Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                       cdna@resgen.com
Seq primer: T7.
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COMMENT
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COMMENT

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Gaps

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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, got to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu, Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 12-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryóta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.

( pases 1 to 554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
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     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
                                                                                                                                                                                                                                    52 CAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGG 111
                                                                                                                                                                                                                                                                                166 CAGATGGAGCGCTACATCTTCAAGCGCCGCAACGGTATTTACATTATAAATCTTGGGAAG 225
                                                                                                                                                                                                                                                                                                                                  112 ATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGAC 171
                                                                                                                                                                                                                                                                                                                                                                                    226 ACATGGGAGAAGCTTCATCTCGCTGCTAGGGTCATCGTTGCCATTGAGAATCCCCAGGAC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1007005B11.2EL_Y1 1007 - RescueMu Grid H Zea mays genomic, DNA
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                                                                                                                                   Length 390;
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/cultivar="mixed background W23/A188/B73"
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/clone_lib="1007 - RescueMu Grid H"
/tissue_type="leaf"
dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanford University 855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                               73;
                                                                                                                                   DB 10;
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                                                                                                                                Score 30.2; I
Pred. No. 63;
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ATCATTGTTCAGTCTGCTAGGCCTTAT 312
                                                       92 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: walbot@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:17573721
                                                                                                                                14.7%;
50.3%;
                                                       122 c
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                                                                                                                                                                                  74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                          Best Local Similarity
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                                                       91 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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                                                                                                                                   Query Match
                                                         BASE COUNT
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BH408584
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                                                                                                                                                                                                                      quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using of 70 c 55 g 72 t 12 others
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Loteae,
                                                                                                                                                /clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lotus japonicus"
/db xref="taxon:34305"
/clone="wWM085068 r"
/clone=lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 390)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AGGICCAIAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGTIAI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 ACAGATAAAAAACGGGTGANTTTTATATCAAATAGACGAAAATGCCCCTNTNGGCGACG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 GCGGATACAAGCAAGACGCTGAAGCTGGAGAGGTACAATAGCTACCTCCGGAAGATTCAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AGCACCAAAGTICICAACGNIICICCIAAAGINNIITIICCCGGGCAACGGIIICINGIAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV427714 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM085e08_r 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 30.2; DB 14; Length 3
45.7%; Pred. No. 56;
Live 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Kazusa DNA Research Institute
                                                    organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 bp
                                                                              /strain="var columbia"
                                                                                              db xref="taxon:3702"
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DNA Res. 7 (2), 127-130 (2000)
20277479
  Location/Qualifiers
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                                                                                                                             clone="240K9T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 390
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FEATURES
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88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: plammers@nmsu.edu.
                                                                                                                                                                            BE604036.1 GI:11067736
                                                                                                                                                                                                           Glomus intraradices.
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Matches 68; Conserv
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ORGANISM
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                                                                        RESULT 52
BE604036/c
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                                                                                                                                                              ACCESSION
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 566)
                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007005. column: 2
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                       BH408577 566 bp DNA linear GSS 12-DEC.
1007005A10.2EL_y1 1007 - RescueMu Grid H Zea mays genomic, DNA
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                                                                                       136 AATGCTTTGAAGAAGCCAAAGAGTCCTATCATGCCAGCTTAGCACAGGATATCAGCACAT 195
                                Gaps
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                                                          28 AGTICTIGGICAATITICCAGGACACAGAIGATICGGICCAAGAACAGGAIAATAGAACTA 87
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 Length 554;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
   DB 17;
                             43;
                                                                                                                                          196 AGCGTGAGAGACAAATAGGATGAAGTGCAGCCAAACTT 234
                                                                                                                   88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAACTT 126
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ch 14.7%; Score 30.2; Dl
1 Similarity 56.6%; Pred. No. 75;
56; Conservative 0; Mismatches
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Pred. No. 75;
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56.6%;
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Best Local Similarity
Matches 56; Conserva
Query Match
Best Local Similarity
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BH408577.1
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Matches
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VERSION
KEYWORDS
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                           RESULT 51
BH408577
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/tissue_type="germinating spore tissue"
/dev_stage="l0 days after germination"
/lab host="E. coli BM 25.8"
/note="Vector: Lambda Triplex2; Site_1: SfilA; Site_2:
SfilB; Spores were germinated in the presence of 1% CO2.
At 10 days, tissue was ground in liquid nitrogen with sand and mRNA isolated with a modified hot phenol/SDS method.
The SMARN-PCR method (Clontech) was used for cDNA synthesis from 1 ug of total RNA followed by directional cloning in Sfil idgested Triplex2 vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end with the 5'Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing primer (Tpx) and the 3' end with the Triplex sequencing princernal primer (Tpx) and the 3' end with the Triplex sequencing t
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                                                                                                                                                                                                                                                                                                             BE604036 SA Lambda-Triplex, 10 day germinating spore library Glomus intraradices cDNA clone GS419-T7, SFI=600 bp 609 609 582, mRNA
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/clone="G8419-T7, STI=600 bp 609 609 582"
/clone_lib="GS Lambda-Triplex, 10 day germinating spore
library"
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Hernandez-Sebastia, C., Allen, J.W., Douds, D.D., Pfeffer, P.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Zygomycota; Zygomycetes; Glomales; Glomaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Peter Lammers
New Mexico State University
Box 30001, MSC 3MLS Horseshoe Drive Las Cruces, NM 88003, USA
TT: 505-646-3918
Fax: 505-646-6846
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207 AGGCGTGAGAGACAATAGGATGAAGTGCAGCCAAACTT 245

    .582
    /organism="Glomus intraradices"

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50.4%; Pred. No. 76;
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be09c01.91 Human Retina CDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone he09c01 5', mRNA sequence.
                             GSS 27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                        Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                          HS 5448 B2 E12 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1024 Col=24 Row=J, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CAGGGTTTGGAGCTTGAGGCCCTCCTGGAGACCCTCGANCACNCATTGGAGACGCTCCAA 64
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 476)
                                                                                                                                                                                                                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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/clone="Plate=1024 Col=24 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
JOI Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                             DNA
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                          476 bp
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                             AQ757100.1 GI:5621903
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                                                                                                                                                                                                           Homo sapiens
                             AQ757100
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                                                                                                                                                                                   human.
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                                                DEFINITION
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                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                           AUTHORS
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KEYWORDS
AQ757100
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BcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
126 c 152 g 160 t 2 others
                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 629)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Praser,C.M.
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                                                                          GSS 21-DEC-1999
                                                                                                RPCI-23-268D24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-268D24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhacetyg. org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 268 row: D column: 24
Seq primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 ACCTGTCTTGAAAATGACACAGAATTTATACTTAGCCCCATGAAAGTTCTGAGGCTAA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GACGIATACGAGIICTIGGICAAITICCAGGACACAGAIGAIICGGICCAAGAACAGGAI 77
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                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Other GSSs: RPCI-23-268D24.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23
                                                                          DNA
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50.7%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-26BD24"
/clone_lib="RPCI-23"
                                                                          629 bp
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                                                                                                                                                                           AQ932853.1 GI:6621959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 CAAGCACATACATGTTCAAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                           DNA sequence.
                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                           house mouse.
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                                                                          AQ932853
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                     RESULT 53
AQ932853/c
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KEYWORDS
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
Do Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 bp DNA linear GSS 30-NOV-2001
CH230-179016,TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-179016, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.

Tat BAC BAC Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-179016.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue From day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 CAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 ACTCCAAAGAAGGAGTGCTCTACAAACGGCTTTTACTCACTACGAAAGTTCTTGGGATAAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 rgrórtrahartrhgacrgaacggrocataggargrcgrancargccagccarrgarca 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 12; Length 519;
Pred. No. 84;
0; Mismatches 60; Indels
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC_IPIG"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: E column: 21
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 9
                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                             and -minmatch 12 options.
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.6%;
1 Similarity 52.4%;
66; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 631)
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and 30
and Keele, J.W.
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Best Local Similarity
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BH305658
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                                                                                                                       Wistow.G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Eye; Vector: pSPORTI; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammania; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 519)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pSPORTI vector (Life Technologies) was constructed at the bloserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pgAcTrAGTATCGAGGGGGGGGGCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Human Retina cDNA (Un-normalized, unamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 ACCAATGACATGGATAATTTAGAGTACTATTATTTTTGTCTACCACACAGAGTATGTCCTC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
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303302 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG384279
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                                                                                                                                                                                                                                                                                                        Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: graeme@helix.nih.gov
Plate: 09 row: c column: 01
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                               National Eye Institute
6/331, N1H, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="he09c01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="Retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="Adult"
/lab_host="EMDH10B"
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                                                                                                    (bases 1 to 513)
                                                                                                                                                                                                                                                                                Contact: Wistow G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                             Homo sabiens
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                                                                                                    REFERENCE
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/db_xref="taxon:4565"
/clone="TaE25010F12R"
/clone_lib="TaE25"
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/clone="Sm1-45018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ250036.1 GI:20445912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AACAGTATAATGGATCAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AACAGGATAATAGAACTA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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BQ250036/c
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          Email: szhao@tigr.org

Clones are derived from the rat BAC library CHOR1-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: 17
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Sml-45018.TR Sml Schistosoma mansoni genomic clone Sml-45018, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 697)
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction
                                                                                                                                                                                                                                                                                                                            /clone="CH230-179016"
/clone=1b="CH230-179016"
/clone=1b="CHOR1-230 Segment 1"
/sex="Female"
/cell type="Brain"
/note="Vector: pTARBAC2.1; Site 1: EcoR1; Site 2: EcoR1;
CHOR-230 Rat (BN/SeNHsd/MCW) BAC library produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea,
Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 TAATATAACTATTCAATAAAATTAAAATTGTCTTCATATACTTCTAACTTACTCTTACAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 t
                                                                                                                                                                                                                                                                                       strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                             /db xref="taxon:10116"
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/db_xref="taxon:6183"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 ÁTÁTATCTÁTÁATTTTAC 271
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                                                                                                                                                                                                     Class: BAC ends.
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/close_lib="Sml" | /close_lib="Sml" | /close_lib="Wetor: pBeloBACI1; Site_1: Hin dIII; Constructed in the laboratory of Dr. Denis De Pasiler at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBACI1 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 X the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosome mansoni bacterial artificial chromosome library. Genomics 65: 87-94."
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-24604
Fax: (204) 983-4604
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/dev stage="25 days after anthesis"
/dev stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pcMV-SPORT6.0 (invitrogen Technologies);
Site 1: Not1; Site 2: MiuI; mRNA obtained from wheat seeds
of cultivar Glanlea 25 days post-anthesis"
3 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3Q250036 113 bp mRNA linear EST 03-MAY-2002 REES5010F12R TaE25 Triticum aestivum cDNA clone TaE25010F12R, mRNA
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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Plate: 010 row: F column: 12
Seq primer: M13 Reverse.
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14.6%; Score 30; DB 17; Length 69.
Best Local Similarity 61.5%; Pred. No. 97;
Matches 48; Conservative 0; Mismatches 30; Indels
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/cultivar="Glenlea"
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Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digstion. The
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                   64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
                                                             Gaps
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                                                                                                                                          104 TACCACAACTTGTTAATTCATCCTACCATCAATATACAGTTTGGGGGCTATTATGAATAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Mashington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone="GBNOME SYSTEMS CLONE ID: Gm-c1051-3675"
/clone lib="Gm-c1051"
/tissue_type="floral meristematic mRNA"
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                 DB 14; Length 313;
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                                                           37;
Score 29.8; DB
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                                       Pred. No. 76;
0; Mismatches
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Pred. No. 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
                                                                                                                                                                                    124 CTTCCTGTGACTAACAGGTCCATAGTTTT 152
                                                                                                                                                                                                                              44 GCTCCTATGAATATTCTTACAATATCTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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BG406256.1 GI:13312605
                 14.5%;
58.4%;
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Best Local Similarity 49.7%;
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
Contact: Dr. Stephen Moore
Det of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2PS, Canada
111 780 492 0169
Fax: 780 492 4265
Email: smoore@afns.ualberta.ca
Insert Length: 423 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                              342 GTAACCACCTTCAGGGTCATTGCCAACATCATAAAAGAGTCCTCGGAAGTATACAAAAAT 283
                                                                                                                                                                                                                                                                                                                                                282 GGACCTGGGAGTCTTGTCAGGAATTAGGTGGGTATGCATTTTCTGTGGTGGAGCATACGG 223
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/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
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/clone_lib="Bos taurus Omasum #1 library"
/tissue_type="Smooth muscle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GTCCATAGTTTTTCACGACACTTCCAAGGACGC 173
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BM433714.1
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                                                                                                                                                                                                                                                                                     /db_xref="taxon:9913"
/clone="E10V013G05"
/clone lib="Bos taurus ovary fetus"
/tissue_type="ovary"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
      Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pZL1; Site 1: S
was deleted from a Not1 site"
111 c 126 g 177 t
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                                                                                                                                                                                                                                                                      /organism="Bos taurus"
                                          Contact: Yoshikazu Sugimoto
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                                                                                                                                                                                                                                            Merrick,J.M., Osman,A., LoVerde,P.T., Chandra,I., Glodek,A., Fraser,C.M. and Lee,N.H.
Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome
                       EST 27-AUG-1999
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Establishment of a high throughput EST sequencing system using poly (A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mamalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .539
/organism="Schistosoma mansoni"
/db xref="taxon:6183"
/clone="SMFAU96"
/clone="SMFAU96"
/clone=lb="Schistosoma mansoni female, Phil LoVerde/Joe Merrick"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV617820 SST 28-NOV-20
AV617820 Bos taurus ovary fetus Bos taurus cDNA clone E10V013G05
                   A1975607 539 bp mRNA linear EST 27-AUG-EST270201 Schistosoma mansoni female, Phil LoVerde/Joe Merrick Schistosoma mansoni cDNA clone SMFAU96 5' end, mRNA sequence.
                                                                                                                                                                               Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

    (bases 1 to 539)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 AGAAAGAGAAATTCAACTCTTAAAGCTAATTTAATTCAGATTGAAGAAGAAAAATGC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 CTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 Trarcaaacaadecrreacarrrrarcererrachraacaacereaacrreaacea 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Indels
                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nhlee@tigr.org
Seg primer: M13 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
Contact: Norman H. Lee
                                                                                                    AI975607.1 GI:5788775
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Local Similarity 51.9%;
                                                                                                                                          Schistosoma mansoni
Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 GAGGGATTT 523
                                                                                                                                                                                                                                                                                                            Gene Index
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ORGANISM
                                        DEFINITION
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                                                                                 ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                              JOURNAL
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AI975607
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Shoemaker,R., Kehn,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF009213 587 bp mRNA linear EST 06-DEC-2001 ss75e02.yl Gm-c1062 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1062-2259 5' similar to TR:Q9ZW45 Q9ZW45 F17L21.24. ;, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AGGTTGTAATCATCCTCCCTTTTCACATGAGTGTTTATGAGAACTGTGGAATGTTTAAA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 ACAAACTTGAAATCTATGGGAAGGGAAAGGGCAAAAGCCTTTCTAAAAACCTACAGTTCTGCA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-56725
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                       Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.5%; Score 29.8; DB 10; Length 581;
Best Local Similarity 48.5%; Pred. No. 1e+02;
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Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from washington University Genome Center. Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. This Sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merrick,J.M., Osman,A., LoVerde,P.T., Chandra,I., Glodek,A., Fraser,C.M. and Lee,N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site 1: BCORI;
Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1976453 637 bp mRNA linear EST 27-AUG-EST271047 Schistosoma mansoni female, Phil LoVerde/Joe Merrick Schistosoma mansoni cDNA clone SMFBF09 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 ACAAACTIGAAAICTAIGGGAAGGGAAGGAGAAAGCCIIICIAAAAACCIACAGIICIGCA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
1 (bases 1 to 637)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 AGGTTGTAATCATCCTCCCCTTTTCACATGAGTGTTTATGAGAACTGTGGAATGTTTAAA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 29.8; DB 12; Length 593; 48.5%; Pred. No. 1e+02;
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Tel: 301 838 3529
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                                                                                                                                                                  FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 593 Std Brror: 0.00
Plate: BP250021820 row: F column: 12
Seq primer: AGCGGATAACAATTTCACACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
/clone="BP250021B20F12"
                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 593.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  organism="Bos taurus"
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Email: nhlee@tigr.org
Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         /ADDIANCE TO Bluescript II SK+; Site 1: ECORI; Site 2:
XhoI; The CDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. ECORI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoRRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."
                             South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 1153 Std Error: 0.00 High quality sequence stop: 405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 217 333 5998
Rex: 217 - 244 5617
Email: h-lewinGuiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
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1 (bases 1 to 593)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF042233 593 bp mRNA linear EST 10-OCT-20
BP250021B20F12 Soares normalized bovine placenta Bos taurus CDNA
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           This clone is available through: ResGen, Invitrogen Corp. 2130
                                                                                                                                                                                                                                                                                                              /tissue type="stem tissue of greenhouse grown plants"
/dev stage="1 month old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 GTAACCACCTTCAGGGTCATTGCCAACATCATAAAAGAGTCCTCGGAAGTATACAAAAAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GGACCTGGGAGTCTTGTCAGGAATTAGGTGGGTATGCATTTTCTGTGGTGGAGCATACGG 132
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                                                                                                                                                                                                                            /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1062-2259"
/clone_lib="Gm-c1062"
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Pred. No. 1e+02;
0; Mismatches 77; Indels 0;
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                                                                                                                                                                                                     /organism="Glycine max"
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Unpublished (2000)
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BF046370 664 bp mRNA linear EST 10-OCT-2000 BP250021A20A7 Soares normalized bovine placenta Bos taurus cDNA clone BP250021A20A7 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 664) Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
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                                                 113 TTGGCAACAAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACG 172
                                                                                                58 TTGGTACTGAACTTCTTGTATTTGGAAAGGCAATAGAGTCTCATGTCATCTACAATACA 117
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/clone="BP250021A20A7"
/clone liber_Soares normalized bovine placenta"
/sex="female"
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Best Local Similarity 48.5%; Pred. No. 1.1e+02;
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High quality sequence stop: 664.
Location/Qualifiers
    Mismatches
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BACKWARD: ATTAACCTCACTAAAG
Insert Length: 664 Std Errox
Plate: BP250021A20 row: A co
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
                                                                                                                                            173 CCATACCGAACAAGCAAGGT 193
                                                                                                                                                                                         118 GCATCCTGACCAACTCATGGT 138
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/tissue_type="callus"
/dev stage="25-40 days old"
/lab_host="Yector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
/hote="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                       ·.
                                                                                                                 /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
; directionally cloned cDNAs"
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning
C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
                      /clone="SMFBF09"
/clone_lib="Schistosoma mansoni female, Phil LoVerde/Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1421295
638 bp mRNA linear EST 16-AUG-20 EST531961 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC66B13 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                             395 AGAAAGAGAAATTCAACTCTTAAAGCTAATTTAATTCAGATTGAAGAAGAAAAAATGC 454
                                                                                                                                                                                                                                                                                                                              68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                            128 CTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 Trarcaacaadadcirgacarrirrarccrerracirraadaadcagaacrreadacreca 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: https://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                     Length 637;
                                                                                                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4081"
/clone="cLEC66813"
/clone_lib="tomato callus, TAMU"
                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                   Score 29.8; DB 9;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                  0; Mismatches
/db xref="taxon:6183"
                                                                                                                                                           136 g
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                                                                                           /sex="female"
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51.9%;
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C
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Bust Local Similarity
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/note="Organ: placenta; Vector: pT7T3Pac; Site_1: BcoRI; Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AGGITGIAATCATCCTCCCTTTTCACATGAGTGTTTATGAGAACTGTGGAATGTTTAAA 543
                                                                                                                                                                                                                                                                                                                                       Gaps
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Score 29.8; DB 13; Length 638; Pred. No. 1.1e+02;

14.5%;

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI; directionally cloned cDNAs" 109 c 154 g 184 t
                                                                                                                                                                                                                                                                                                                                                          Schistosoma mansoni
Stukaryota: Metazota; Platyhelminthes; Trematoda; Digenea;
Strigedidia; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 712)
Merrick, J.M., Osman, A., LoVerde, P.T., Cho, J., Fraser, C.M. and Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Schistosoma mansoni female, Phil LoVerde/Joe
Merrick"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome
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88 AGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATGGCAACAACTTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 agaaagaaaaatrcaacrcrtaaagcraatrraatrcagatrgaagaagaaaaaaaatgc 454
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                                     544 ACAAACTTGAAATCTATGGGAAGGGAAAGGAGAAAGCCTTTCTAAAACCTACAGTTCTGCA 603
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                                                                             148 GITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGIT 196
                                                                                                                    604 TITIGGACTCCTGACTTTCTCAGTCTACAGAGATTATAACAAGACATT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Norman H. Lee
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3529
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Schistosoma mansoni"
/db_xref="taxon:6183"
/clone="SMFBX14"
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Seg primer: M13 reverse.
Location/Qualifiers
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GSS.
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Unpublished (2001)
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/Globe_lib="moutiness" / Globe_lib="Entamones histolytica Sheared DNA" / Glone_lib="Wector: pH0S1; Site_!: Bat I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kD). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, U.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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BQ064772
BQ064772.1 GI:19893720
EST.
                                                                                                                                                                                                 Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
Department of G. Everyotic Genomics
9712 Medical Center Dr., Rockville, MD 20850, USA
TTel. 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library. M13-Reverse
Class: shotgun
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 944)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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    944
/organism="Entamoeba histolytica"

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High quality sequence stop: 299.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Yosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 454)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab.,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH633544 4 454 bp DNA linear GSS 01-FEB-2002
SALK 042739 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thalīana genomic clone SALK_042739, DNA sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of TDNA. This sequence lies within within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 AAGGAGGGTTATGATTACTGGGTCGATGACCGTTAGATTGCCAATTCGACGGAGGAAAAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 GATTATTGACGGTAGGACCAATGGCTGCGATGGCTGGATCGAGAGCGAATGACTGATGAT 270
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        A Sequence-Indexed Library of Insertion Mutations in the
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                                                                  Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Columbia 0"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                             Email: ecker@salk.edu
                                 Arabidopsis Genome
Unpublished (2001)
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Class: TDNA tagged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="INAGE:995529"
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/clone=lib="NIH MGC-99"
/lissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph, Vector: pOTB7; Site_1: Xho1; Site_2:
RooRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xho1 sites using the following 5' adaptor:
GGCAGGG(G). Size-selected >SOODp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH633508 42693 Arabidopsis thaliana TDNA linear GSS 01-FEB-2002 SALK 042693 Arabidopsis thaliana genomic clone SALK_042693, DNA sequence.
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Abnoso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thale cress. Arabidopsis thaliana Exabidopsis thaliana Eukaryota; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                       Email: cgapber@mail.nih.gov
Tissue Procurement: Lou Standt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information activity://image.lln.gov
Phttp://image.lln.gov
Phate: LiCM2099 row: p column: 18
High quality sequence start: 16
High quality sequence stop: 641.
                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               939 AİGCCCİCGAAĞİTİTTİTİTİTİTİTİTİTİAAAAAAAAAGAIGTITATTIAGGAA 880
                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 29.8; DB 14; Length 1002; 49.7%; Pred. No. 1.3e+02; Live 0; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 GTGACTAACAGGTCCATAGTTTTTCACGACACT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 GTGATGCAAAGCTGAAGTTGTGTGTACAAGACT 787
                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 g
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1 227 c
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                                                                                                                                                          Unpublished (1999)
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  Homo sapiens
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Gaps

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ыличазу 474 bp mRNA linear EST 13-JUN-2001
MR4-HN0054-060301-003-g11 HN0054 Homo sapiens cDNA, mRNA sequence.
BI004390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HN0054-060301-003-gl1&t3=2001-03-0&t4=1)
Seq primer: puc 18 forward
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0
                                                                                                                                                                                                                                                                 /db xref="taxon:3702"
/clone="SALK 042739"
/clone="SALK 042739"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 474)

                         This is single pass sequence recovered from the left border of TDNA. This sequence lies within within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 AAGGAGGTTATGATTACTGGGTCGATGACCGTTAGATTGCCAATTCGACGGAGGAAAAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 GATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GATTATTGACGGTAGGACCAATGGCTGCGATGGCTGGATCGAGAGCGAATGACTGATGAT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 ATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 14.4%; Score 29.6; DB 17; Length 454; 1 Similarity 51.5%; Pred. No. 1.1e+02; 68; Conservative 0; Mismatches 64; Indela n.
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                                                                                                                                                                                                          'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                              /strain="Columbia 0"
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI004390.1 GI:14408464
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Email: ecker@salk.edu
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                                                                                                                   Class: TDNA tagged
                                                                                                                                                                          .454
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Matches 68; Conserv
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                                                                                      At 2945620
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/db xref="rexon:9606"
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/clone_lib="HN0054"
/clone_lib="HN0054"
/note="Organ: head normal; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analysis of expressed sequence tags from subtracted and unsubtracted C. felis hindgut and Malpighian tubule cDNA libraries (Unpublished (2001) Contact: Gaines, Patrick J. Pharmaceutical Discovery Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 498)
Gaines,P.J., Brandt,K.S., Eisele,A.M., Wagner,W.P., Bozic,C.M. and Wisnewski,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="hindgut and Malpighian tubule subtracted cDNA
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/tissue type="hindgut and Malpighian tubule"
/dev_stage="unfed adult and 24 hour cat blood-fed adults
(1:1 ratio)"
/note="The library was made using the PCR-Select( cDNA
Subtraction kit (CLONTECH Laboratories, Inc.) with 2 (9
hindgut and Malpighian tubule mRNA used as to make the
'tester' cDNA and 2 (9 carcass (all flea tissues minus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 CAGGATAATAGAACTAAGCAACGATACAATTTGGGTGGATTGGCAACAAACTTCCTGT 131
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498 bp mRNA linear EST 01-AUG
3092-33 hindgut and Malpighian tubule subtracted cDNA library
Ctenocephalides felis cDNA clone 3092-33, mRNA sequence.
BF731738
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Neoptera, Endopterygota, Siphonaptera, Pulicidae, Pulicinae,
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0
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1 Similarity 59.5%; Pred. No. 1.1e+02;
50; Conservative 0; Mismatches 34; Indels 0;
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Tel: 970 493-7272
Fax: 970 472-1644
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Seq primer: CGA GCT CGG ATC CAC TAG.
                                                                                                               /organism="Homo sapiens"
High quality sequence start: 32
High quality sequence stop: 228.
Location/Qualifiers
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/clone="3092-33"
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the hindgut and Malpighian tubules) to make the 'driver' cDNA. Suppression PCR and subtractive hybridization techniques are then used to enrich for cDNAs in the tester pool that are not also present in the driver pool.

9 others 88 g 153 t 84 C 164 a BASE COUNT ORIGIN

0; Gaps Query Match
14.4%; Score 29.6; DB 12; Length 498;
Best Local Similarity 54.6%; Pred. No. 1.1e+02;
Matches 53; Conservative 0; Mismatches 44; Indels 0;

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Search completed: February 15, 2003, 23:10:31 Job time : 1202 secs

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February 11, 2003, 08:36:01; Search time 29 Seconds (without alignments) 404.989 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Q26566 schistosoma
O75851 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97400522; PubMed=9252357; Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.; Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.; Identification and Sequence Analysis of Two New Members of the SKALP/elafin and SPAL-2 Gene Family, Blochemical Properties of the Transglutaminase Substrate Motif and Suggestions for a New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BTRAPPIN-2.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zeeuwen P.L.J.M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UNN-1998 (TrEMBLrel. 06, Created)
01-UNN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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J. Biol. Chem. 271:7012-7018 (1996).
EMB.; AJ22316; CAA11184.1;
HSSP; P19957; 2REL.
HSSP; P19957; 2REL.
InterPro; IPR000737; Squash.
InterPro; IPR002098; SVP_I.
InterPro; IPR00201; SVP_I.
InterPro; PR00059; Wap. 1.
PRINTS; PR00003; 4DISULPHCORE.
'PRINTS; PR00293; SQUASHINHETR.
SMART; SM00217; WAP; 1.
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J. Biol. Chem. 272:20471-20478(1997).
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MEDLINE=93280175; Pubmed=7685029;
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NCBI_TaxID=9913;
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MEDLINE=98391820; PubMed=9722657;

MEDLINE=98391820; PubMed=9722657;

Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;

Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;

Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;

Enterpole Medical Sequence of the trappin multigene family in the Suidae.";

EMBL, AB003281; BAA77825.1; -.

R HSSP, P19957; 2REL.

R HSSP, P19957; 2REL.

R InterPro; IPR00037; Squash.

R InterPro; IPR00095; wap; 1.

R PRINTS; PR00095; wap; 1.

R PRINTS; PR00093; SQUASHINHBTR.

R PRINTS; PR00137; WAP; 1.

R PROSITE; PR00137; 4 DISULFIDE_CORE; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phacochoerus aethiopicus (Warthog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Phacochoerus.
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                                                                                                         134 AA; 14324 MW; CDC7C13D4228A955 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
PROSITE; PS00313; SVP_1; 2.
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                                                                                                                                                                                                                  Local Similarity 67.7%
les 42; Conservative
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Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=85517;
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                                                                       NON TER
SEQUENCE
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                                                                                                                                                                                                                                                        Matches
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       SY PR
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MEDLINE=98391820; PubMed=9722657;
Purutani Y.; Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
Purutani Y.; Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
J. Biochem. 124:491-502(1998).

Biochem. 124:491-502(1998).

EMBL; AB003283; BAA77827.1; -.
HSSP; P19957; 2REL.

InterPro; IPR002073; Squash.
InterPro; IPR002098; SVP_I.

InterPro; IPR002221; WAP.
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                                                                                                     "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QEPVKGP-----VSTKPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Tayassuidae; Pecari.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.2%; Score 216.5; DB 6; Length 143; 60.3%; Pred. No. 1.2e-21; Live 5; Mismatches 13; Indels 7;
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                                    MEDLINE=96215132; PubMed=8636131;
Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
                                                                                                                                                                                                       Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A., Tachibana S., Hirose S.; J. Biol. Chem. 0:0-0(0). Biol. Chem. 0:0-0(0). EmBL; D0322; BAA08857.1; -. EMBL; D83668; BAA12038.1; -. HSSP; P19957; ZREL.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00095; wap; 1.
PRINTS; PR00095; wap; 1.
SMART; SM00217; WAP; 1.
PROSTTE; PS00317; WAP; 1.
SEQUENCE 143 AA; 15373 MW; 4D6CAAC205B9FC82 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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PROSITE; PS00313; SVP I; UNKNOWN 2.
NOW TER
                                                                                                                          members.";
J. Biol. Chem. 271:7012-7018(1996)
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PRINTS; PR00003; 4DISULHCORE.
PRINTS; PR00293; SQUASHINHETR.
SMART; SM00217; WAR; 1.
                                                                                                                                                                                         SEQUENCE OF 29-143 FROM N.A.
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Best Local Similarity 55.6%
Matches 35; Conservative
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Best Local Similarity
                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trappin (Fragment)
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SEQUENCE
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Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J., Wieringa B., Schalkwijk J.; "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97400522; PubMed=9252357;
Zeetwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
Zeetwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
Identification and Sequence Analysis of Two New Members of the SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the Transglutaminase Substrate Motif and Suggestions for a New
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
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Pred. No. 3.5e-17;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeeuwen P.L.J.M.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                           89 AA.
                                                                                                                                                                                                                                                                                                                                                                                       STrappin-2 protein precursor (Fragment).
STRAPPIN-2.
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J. Biol. Chem. 272:20471-20478(1997).
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J. Biol. Chem. 268:12028-12032(1993).
EMBL; AJ723215; CAAl1183.1; -.
HSSP; P19957; 2REL.
                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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J. Biol. Chem. 271:7012-7018(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque)
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1 Similarity 97.1%;
33; Conservative
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InterPro; IPR002221; WAP.
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PROSITE; PS00313; SVP_I; 2.
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Best Local Similarity
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                                                                                                                                   149 LNP 151
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8; Gaps

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MEDLINE=89391820; PubMed=9722657;
MEDLINE=89391820; A. Yasue H., Alexander L., Beattie C., Hirose S.;
"Evolution of the trappin multigene family in the Suidae.";
J. Biochem. 124:491-502(1998).
EMBL; AB001282; BAA77826.1; -.
HSSP; P19957; 2REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QEPVKGPVS-----TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Elafin family member protein precursor.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            Phacochoerus aethiopicus (Warthog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Phacochoerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 181.5; DB 6; Length 207; 47.6%; Pred. No. 9.2e-17; Live 10; Mismatches 16; Indels 7;
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Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AA; 22352 MW; 0D7AD530105F0A45 CRC64;
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AA.
                                                                                                                                                    207 AA
                  56 PVKGPVSTKPGSCPNILIRCAMLNPPNRCLKDTD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00317; 4 DISULFIDE CORE; 1.
                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                  PRT;
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J. Biol. Chem. 271:7012-7018(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00293; SQUASHINHETR.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000737; Squash.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                            SPAI (Trappin-1) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 47.68
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=85517;
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SEQUENCE
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                                                                                                    RESULT 6
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Secretory leukocyte protease inhibitor.
Eattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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HSSP, P19957; ZREL.

InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AQPPVQGRLLHYKPGLCPWIFLRCPLPKPPNKCWRDSHCPGVMKCCEGFCGNECSYPR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 20, Last annotation update)
Trappin-6 (Fragment).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AOEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
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                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.3%; Score 171; DB 11; Length 131;
52.8%; Pred. No. 1.6e-15;
tive 4; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                       121 181 POTENTIAL.
181 AA; 19972 MW; 90A3F88638C0A1D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.3%; Score 177.5; DB 6; Best Local Similarity 51.7%; Pred. No. 2.8e-16; Matches 30; Conservative 9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA.
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                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                    PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=99380355; PubMed=10449524;
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J. Biochem. 124:491-502(1998).
EMBL; D50323; BAA08858.1; -.
HSSP; P19957; 2REL.
                                                                                                                                        PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
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PRINTS, PR00003, 4DISULPHCORE.
ProDom, PD001224, WAP, 1.
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Best Local Similarity 52.8%
Matches 28, Conservative
                                                                             InterPro, IPR002221; WAP.
Pfam, PF00095; wap, 1
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Protease.
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                     Q9WUQ4
Q9WUQ4;
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RESULT 11
            Q9WUQ4
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Best Local Similarity 45.5%; Pred. No. 1.6e-15;
Matches 30; Conservative 7; Mismatches 19; Indels 10; Gaps
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Purutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
Furutuani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
J. Biochem. 124:491-502(1998).
EMBL; AB011010; BAA28418.1; -.
INESPP. P19957; 2REL.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                   QEPVKGP------VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                        31 ODPVKGODVVVAQDRAGLPFKRGLCPRVRIHCNLWNPPNQCWRDAHCPGAKKCCEGFCGK 90
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordača, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.8%; Score 166; DB 6; Length 180; 53.8%; Pred. No. 1e-14; tive 4; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC
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                                                                                                                                                                                   Last sequence update)
Last annotation update)
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InterPro; IPR0022098; SVP I.
InterPro; IPR002201; WAP.
Pfan; PF00095; wap; I.
PRINTS; PR002003; 4DISULPHCORE.
SMART; SM00217; WAP; II.
PROSITE; PS00317; 4 DISULPIDE CORE; UNKNOWN I.
PROSITE; PS00313; SVP I; 4.
                                                                                                                                   Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SMART; SM0217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hippopotamus amphibius (Hippopotamus).
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                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 28; Conserv
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                                          SEQUENCE FROM N.A.
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                    NCBI TaxID=9913;
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SEQUENCE
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Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Chen D.H., Xu X.P., Bagchi M.K., Bagchi I.C.;
A Chen D.H., Xu X.P., Bagchi M.K., Bagchi I.C.;
A Chen D.H., Xu X.P., Bagchi M.K., Bagchi I.C.;
Twoleular cloning and spatio-temporal expression of rat secretory
I eukcycte protease inhibitor (SLPI) in the uterus.";
I leukcyce protease inhibitor (SLPI) in the uterus.";
I submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
I EMBL, AFISIA921, AAD34035.1;
I REMBL, PRIO02221; WAP.
IN PROPOS; PRISULPHCORE.
IN PRODOUZ24; WAP; 2.
IN SMART; SM00217; WAP; 2.
IN SMART; SM00217; WAP; 2.
IN PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
caltrin-like protein II precursor.
cavia porcealus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae, Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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"Evolution of caltrin-like protein.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 130 AA; 14017 MW; A630BA3FCE3A9D9D CRC64;
                                                                                                                                                        Last sequence update)
Last annotation update)
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SMART; SM00286; PTI; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
130 AA.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S., "Evolution of the trappin multigene family in the Suidae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AQEPVKG-------PVSTKP-----GSCPIILIRCAMLNPPNRCLKD 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
NCBI_TaxID=10141,
                                                                                                                                                                                                                                        Bukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
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                     ch 48.3%; Score 158; DB 11; Length 76; Il Similarity 47.1%; Pred. No. 5.4e-14; 24; Conservative 8; Mismatches 19; Indels
                                                                                     26 GQAINRPGSCPRVMIYCPARHPPNKCTSDYDCPKPQKCCPGYCGKQCYQPE 76
                                                                       7 GPVSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-SEMINAL VESICLE;
Furutani Y., Kawai R., Kato A., Hirose S.;
Guinea pig trappin.";
'Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 2 SEQUENCE 114 AA; 12239 MW; D5F4F6C256C5374E CRC64;
76 AA; 8677 MW; 8B84CFD2FB0B4827 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Elafin homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.3%; Score 135; DB 6; 38.6%; Pred. No. 1.1e-10;
                                                                                                                                                         114 AA
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                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=98391820; PubMed=9722657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 AQCPGFQKCCR-VCGVKSCADPR 114
                                                                                                                                                                                                                                                                                                                                                              HSSP; P19957; ZREL.
InterPro; IPR000737; Squash.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00293; SQUASHINHETR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 TDCPGIKKCCEGSCGM-ACFVPQ 57
                                                                                                                                                                                                                                                                                                                                       J. Biochem. 124:491-502(1998).
EMBL; AB003285; BAA77829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.64
Matches 32; Conservative
                                                                                                                                                         PRELIMINARY;
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                                   Best Local Similarity
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SEQUENCE
                        Query Match
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Rhabditidae; Peloderinae; Caenorhabditis.
                        TISSUE-SEMINAL VESICLE;
MEDLINE-99289296; PubMed=10359639;
Scalkwijk J., Wiedow O., Hirose S.,;
"The trappin gene family: proteins defined by an N-terminal transglutaminase substrate domain and a C-terminal four-disulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 40.1%; Score 131; DB 11; Length 1557; Local Similarity 47.9%; Pred. No. 4.6e-09; les 23; Conservative 8; Mismatches 15; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2%; Score 121.5; DB 4; Length 224; 51.0%; Pred. No. 1.4e-08; tive 5; Mismatches 16; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ211D12.5 (Novel protein containing 2 WAP-type domains.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VSVKLGSCPEDQLRC--LSPMNHLCHKDSDCSGKKRCCHSACGRDCRDP 120
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MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 VSTKPGSCPIILIRCAMLNPPNR-CLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                            EMBL; AB058645; BAB79626.1; -
EMBL; AB058645; BAB79626.1; -
InterPro; IPR002201; WAP. I.
InterPro; IPR00221; WAP. I.
SMART; SM00217; WAP; 1.
SMART; SM00217; WAP; 1.
SMOSTIE; PS00313; 4 DISULFIDE CORE; UNKNOWN_1.
SROSTIE; PS00313; 9 I UNKNOWN 1.
SROSTIE; PS00313; 9 I UNKNOWN 1.
SROUGHCE 1557 AA; I63269 MW; F9047D9B3359C719 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burton J.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6; CAD27771.1; -. 224 AA; 24238 MW; 305CC59024058F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 51.0 tes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C08G9.2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00317; 4 DISULFIDE_CORE; PROSITE; PS00280; BPTI KUNITZ_1; 8. PROSITE; PS50279; BPTI_KUNITZ_2; 10. PROSITE; PS50092; TSP1; 1.
                                              SEQUENCE FROM N.A.
MEDLINE=99457716; PubMed=10528409;
                                                                                                                                                                                                                                                                                                                                                     Kunitz_BPTI; 10
                                                                                                                                                                                                InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                InterPro; IPR004094; Antistasin.
                                                                                                                                                                                                                                                                         Pfam; PF02822; Antistasin; 4.
Pfam; PF00047; ig; 2.
Pfam; PF00014; Kunitz BPTI; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00003; 4DISULPHCORE.
ProDom; PD001224; WAP; 1.
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPT1
SMART; SM00408; IG62; 2.
SMART; SM00131; KU; 10.
SMART; SM00209; TSP1; 7.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                            InterPro; IPR000884; TSP1.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Pfam; PF00095; wap; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBVE57;
                                                                                                                          sexta."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VE57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOOR NEW KWA
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jonather A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Earsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Weinston A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.8%; Score 117; DB 5; Length 2150;
Best Local Similarity 43.6%; Pred. No. 5e-07;
Matches 24; Conservative 7; Mismatches 14; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lacunin precursor.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 PVSTKP---GSCPIILIRCAMINP--PNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2150 AA; 234131 MW; 4ED668D669C7523C CRC64;
                                                                                                                                                                                                                                              "The sequence of C. elegans cosmid C08G9."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0317; 4 ISULFIDE CORE; 9.
PROSITE; PSO0200; BPTI_KUNITZ_1; 1.
PROSITE; PSO0209; BPTI_KUNITZ_2; 1.
PROSITE; PSO0484; THYROGLOBULIN I; UNKNOWN 1.
PROSITE; PSO0484; THYROGLOBULIN I; UNKNOWN 4.
PROSITE; PSO04088; ZINC_FINGER_C2H2_1; UNKNOWN 1.
Serine procease inhibitor.
Serine procease inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004094; Antistasin.
InterPro; IPR004094; Antistasin.
InterPro; IPR002561; EGF-like.
InterPro; IPR002213; Kunitz_BPTI.
InterPro; IPR002221; MAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002899; WRI/EB.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF02822; Antistasin; 6.
Pfam; PF00014; Kunitz_BFI; 1.
Pfam; PF00086; thyroglobulin_1; 6.
Pfam; PF00095; wap; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0003; 4DISULPHCORE.
PRINTS; PRO0759; BASICPPASE.
PRODOM; PD000222; KUMITZ_BPTI; 1.
PRODOM; PD001224; WAP; 4.
                                                                                                                                                                                                                                                                                                                                                   EMBL; AF036687; AAB88311.1; -...
HSSP; P10646; 1ADZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
Geisel C., Stellyes L.;
"The sequence of C. eleg
                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART, SM00131; KU; 1.
SMART, SM00211; TY; 6.
SMART, SM00217; WAP; 9.
SMART, SM00289; WRI; 6.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                        elegans."
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Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
"Expression of lacunin, a large multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7%; Score 113.5; DB 11; Length 126; 44.9%; Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2888 PVN-KTGYCPVEQASTTEYPCPNECVDDADCRGVGKCCARGCGRACAVP 2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL 1 21 POTENTIAL.
SEQUENCE 3198 AA; 349364 MW; AB4ACD459C0D9134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Strausberg R.; Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; Breath AAH19734.1; -. InterPro; IPR002221; WAP. PF00095; wap; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AA; 13839 MW; 8D10353557B2F75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ^ Match 35.6%; Score 116.5; DB 5; Local Similarity 44.9%; Pred. No. 8.5e-07; les 22; Conservative 4; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_2.
                                                                                                                                           Insect Biochem. Mol. Biol. 29:883-897(1999).
EMBL, AF078161, AAF04457.1; -.
HSSP, P12111; 2KNT.
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1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                    262 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00217; WAP; 3.
PROSITE; PS00317; 4_DISULFIDE_CORE; 5.
                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, Created)
                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97400522; PubMed=9252357;
                                                                                                                                                                                                                                                                                                                                                              Ovulatory protein-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002221; WAP.
Pfan; PP00005; Wap; 5.
PRINTS; PR00003; 4DISLPHCORE.
ProDom; PD001224; WAP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Reprod. 0:0-0(1997).
EMBL; U67854; AAB63598.1; -.
HSSP; P19957; 2REL.
                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.18
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                              PRELIMINARY;
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262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
                                                                                                                                                                                                                                             098988;
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                                                                                                                                                      RESULT 21
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د
      Gaps
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ211D12.4 (Similar to Elafin-like protein from mouse and WAP-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21638013; PubMed=11779191;
Lundwall A., Clauss A.;
"Identification of a novel protease inhibitor gene that is highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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CHAIN 24 111 PUTATIVE PROTEASE INHIBITOR WAP2.
SEQUENCE 111 AA; 12050 MW; 2DF839043F1A0997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.3%; Score 112; DB 4; Length 111; Best Local Similarity 42.9%; Pred. No. 1.4e-07; Matches 24; Conservative 6; Mismatches 24; Indels
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                                                                                             75 VFVKSGKCPVDQLRC--LSPTKHMCNKDSDCSGKKRCCASACGRDCRDP 121
                                                           9 VSTKPGSCPIILIRCAMLNP-PNRCLKDTDCPGIKKCCEGSCGMACFVP 56
   7; Mismatches 17; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 233016; CAC36291.2; -.
NON TER 1
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                                                                                                                                                                                                                                                                                                                        expressed in the prostate.";
Biochem. Biophys. Res. Commun. 290:452-456 (2002).
EMBL; AND37803; AAK68848.1;
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
PRINTS; PR0003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
PROSTTE; PS00317; 4 DISULFIDE_CORE; UNKNOWN_1.
                                                                                                                                                                                                                                                                         111 AA.
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Matches 24; Conservative
   Conservative
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22;
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Matches
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Garczynski M.A., Goetz F.W.;
"Modecular characterization of a ribonucleic acid transcript that is
"highly up-regulated at the time of ovulation in the brook trout
(Salvelinus fontinalis) ovary.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
Salvelinus fontinalis (Brook trout) (Brook char).
Mediang Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.8%; Score 110.5; DB 13; Length 262; 43.1%; Pred. No. 5e-07; Indels 17;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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28200 MW; D2EC50FFAFECF807 CRC64;
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Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                            Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J., Wieringa B., Schalkwijk J.; "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes Purification, CDNA Sequence, and Evidence for Transglutaminase Cross-
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Tachibana S., Hirose S.,
"Accelerated evolution in inhibitor domains of porcine elafin family
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BTRAPPIN-5.
BOR taurus (Bornie).
BURAPPIN-5.
BURAPPIN-5.
BURATYOLA: Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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"Identification and Sequence Analysis of Two New Members of the
SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the
Transglutaminase Substrate Motif and Suggestions for a New
SKALP/elafin and SPAI-2 Gene Family, Biochemical Properties of the Transglutaminase Substrate Motif and Suggestions for a New
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                                                                                                                                                                                                                                                                                                                                                       Length 96;
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Pred. No. 4.1e-07;
7; Mismatches 7; Indels
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  10145 MW; 33A8C146E0E6AEC1 CRC64;
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J. Biol. Chem. 272:20471-20478(1997)
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                    Nomenclature.";
J. Biol. Chem. 272:20471-20478(1997)
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J. Biol. Chem. 268:12028-12032(1993)
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                                                                                                                                                                                                                members.";
J. Biol. Chem. 271:7012-7018(1996).
EMBL; AJ22317; CAA11185.1; -.
HSSP; P19957; ZEEL.
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                                                                     MEDLINE=93280175; PubMed=7685029;
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Best Local Similarity 45.5%;
Matches 20; Conservative
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(in) Unknown A. (eds.);
PROCEEDINGS OF THE PIFTH INTERNATIONAL SYMPOSIUM ON THE REPRODUCTIVE PHYSIOLOGY OF FISH, pp.289-289, Unknown Publisher (1995).
EMBL; U03890; AAA03534.1; -.
HSSP; QNOLBS; 1TWP.
HIGHERO; IPROD221; WAP.
PF00095; wap; 2.
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(In) Fujimoto S. (eds.);
FRONTIERS IN ENDOCRINOLOGY - NEW ACHIEVEMENTS IN RESEARCH OF OVARIAN
FUNCTION, pp.183-190, Ares-Serono Symposia, Rome, Italy (1995).
                                                                                                                                                                                                                                                                                                                                                                                       "Accelerated evolution in inhibitor domains of porcine elafin family
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Salvelinus fontinalis (Brook trout) (Brook char).
Salvelinus fontinalis (Brook trout) (Brook char).
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 110;
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Tachibana S., Hirose S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
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110 AA; 11575 MW; 5F9E4D24A21318F2 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.0%; Score 108; DB 6;
42.6%; Pred. No. 4.7e-07;
tive 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                   linking.";
J. Biol. Chem. 268:12028-12032(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    members.";
J. Biol. Chem. 271:7012-7018(1996).
EMBL; AJ22318; CAA11186.1; -.
HSSP; P19957; 2REL.
InterPro; IPR002221; WAP.
SMART; SM00217; WAP; 1.
TISSUE=TONGUE;
MEDLINE=93280175; PubMed=7685029;
                                                                                                                                                                                                                                                                                                   MEDLINE=96215132; PubMed=8636131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
>110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=OVARY;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    rissue=tongue;
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Local 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
inhibitor domain and WAP-type (Whey acidic protein) 'four-disulfide
                                                                                                                                                                                                                                                                                                           Trichosurus vulpecula (Brush-tailed possum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                              28 GGISTAKPGVCP----RRRWGIGICAEL-----CSSDSDCPNDEKCCHNGCGHVCIAP
                                                                                                                                            7 GPVST-KPGSCPIILIR-----CAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 PIKAKPGRCPAIAEVC----PKNMSWIDNCQSDDHCNRSKKCCSSGCGQRCMKP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PVSTKPGSCPIILIRCAMLNPPN-----RCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                               DB 13; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%; Score 105.5; DB 6; Length 188; 38.9%; Pred. No. 1.7e-06; Live 1; Mismatches 23; Indels 9;
                                                                                            32.3%; Score 105.5; DB 13; Length 41.4%; Pred. No. 1.1e-06; tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Demmer J., Stasiuk S.J.;
"Possum whey acidic protein.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275311, AAK69407.1;
InterPro; IPR002221; WAP.
Fram, PF00095; wap; 3.
ProDom, PD001224; WAP; 1.
PROSITE; PS00317; 4 DISULPIDE CORE; UNKNOWN 3.
SEQUENCE 188 AA; 20626 MW; 71FE8B8572E0ĀASA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                      121 AA; 12735 MW; F407403777B4D3FE CRC64;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            PRT; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 232 AA.
                                                            POTENTIAL.
          ProDom; PD001224; WAP; 1.
SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LACTATING MAMMARY GLAND;
 PRINTS; PR00003; 4DISULPHCORE
                                                                                                         Best Local Similarity 41.4 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 21; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                      Whey acidic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                      SEQUENCE
                                                                                               Query Match
                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96A34;
                                                            IGNAL
                                                                                                                                                                                                                            Q95JH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96A34
                                                                                                                                                                                                      RESULT 25
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                                                                                                                                                                                                                Db
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S T W D R
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RA Adams M.D., Ceniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F., R. George R.A., Lewis S.E., R.Cihards S. P. Ashang O., Chen L.X., Ratton G.G., Worthman J.R., Aghards S.E., R. Ashang O., Chen L.X., R.A. Sutton G.G., Worthman J.R., Anderer E.G., Helt G., Nelson C.R., Miklos G.L.G., R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D., R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D., R.A. Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.M., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center P., Center P. R.A. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center P., Doutchan W., Bouch E.S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Fosler C., Gabriellan E., Gelbart W.M., Glasser K., R.A. Hostin D., Houston K.B., Gorrell J.H., Gu Z., Guan P., Harris N.L., Harvey D., Heanan T.J., Hernandez J.R., Houck J., RA. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Martie B.E., Kodira C.D., Kraft C., Kravitez S., Kulp D., Lai Z., Lai M. Mushy, B., Murphy E., Murchy D.M., Nelson D.L., Marchi W. Murphy B., Murphy L., Muzny D.M., Nelson D.L., R.A. Mount S.M., Moy M., Murphy B., Murshy D.M., Nelson D.L., R.A. Rhimmel B.E., Shen H., Salue B.C., Siden-Kiamed T., Sucheler F., Shen H., R. R. Spier E., Shen H., Shier E., Shen H., Shier E., Shen H., Shier E., Shen H., Shier E., Shen H., Shier E., Shen H., Shier R., Shen H., Shier E., Shen H., Shier R., Shier E., Shen H., Shier R., Shier E., Shen H., Shier R., Shier E., Shen H., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier E., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shier R., Shie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBL_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 31.5%; Score 103; DB 4; Length 23 Local Similarity 37.5%; Pred. No. 4.6e-06; es 18; Conservative 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 STKPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
Stavrides G.S., Huckle E.J., Deloukas P.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL AL031663; CAB37634_2; --
EMBL; AL5917165; CAC39449-1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA; 26806 MW; 2B0ACF9FEF4D66F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                 pfam; PF00095; wap; 3.
ProDom; PD00022; Kunitz BPT1; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 3.
PROSITE; PS00209; BPTI KUNITZ 1; UNKNOWN 1.
PROSITE; PS00209; BPTI KUNITZ 2; 1.
Hypothetical protein; Serine Protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                  InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002221; WAP.
Pfam; PF00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG5639 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VB21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
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NCBI TaxID=9606;
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            097751;
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

BNBL, AE003761; AAF56722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95083703; PubMed=7991635;
Drake L., Korchev Y., Bashford L., Djamgoz M., Wakelin D., Ashall F.,
Bundy D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 PVPACLPRKPGQCPYLV-----PPGPDNLDANTCAYECRTDAHCDGARRCCSNGCGTQ 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PVKGPVSTKPGSCPIILIRCAMLNPPN------RCLKDTDCPGIKKCCEGSCGMA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The major secreted product of the whipworm, Trichuris, is a pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.5%; Score 103; DB 5; Length 15: Best Local Similarity 30.8%; Pred. No. 2.8e-05; Matches 20; Conservative 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00317; 4 DISULFIDE CORE; 2.
PROSITE; PS00022; EGF 1; UNKNOWN 3.
PROSITE; PS00484; THYEQCADBULIN I; 3.
PROSITE; PS00678; WD REPEATS 1; UNKNOWN 1.
SEQUENCE 1511 AA; 165894 WW; BD44D64CB9DCC3B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Barker G.C., Bundy D.A.P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036161; AAC04763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forming protein.";
Proc. R. Soc. Lond., B, Biol. Sci. 257:255-261(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     InterPro; IPR004094; Antistasin.
InterPro; IPR000561; EGF-like.
InterPro; IPR003645; Folv.
InterPro; IPR002223; Kunitz BPTI.
InterPro; IPR000716; Thyroglobulin_1.
InterPro; IPR0002221; WAP.
InterPro; IPR001680; WAP.
InterPro; IPR001689; WRI/EB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00274; FOLN; 3.
SMART; SM00131; KU; 1.
SMART; SM00211; TY; 5.
SMART; SM00211; TY; 5.
SMART; SM00217; WAP; 2.
SMART; SM00289; WRI; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02822; Antistasin; 4.
Pfam; PF00086; thyroglobulin_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00003; 4DISULPHCORE.
                                                                                                                                                                                                                                                 FlyBase; FBgn0039527; CG5639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative porin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichuris trichiura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00095; wap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                827 CVDPQ 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 CFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    044397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 QPVNGTVSRTKPGSCP----PSPLGPVGLALFCOTDIDCEGSMKCCMTIVGYECTPPQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EPVKGPVS-TKPGSCPIILIRCAMLNPPNR---CLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SIMPLINES BAS88243, PubMed=2969454;

Simmen R.C.M., Baumbach G.A., Roberts R.M.;

"Molecular cloning and temporal expression during pregnancy of the messenger ribonucleic acid encoding uteroferrin, a progesterone-induced uterine secretoxy protein.";

Mol. Endocrinol. 2:253-262(1988).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                            Length 903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 STKPGSC-PILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 SLKGGACPPRKIVQCLRYEKP-KCTSDWQCPDKKKCCRDTCGIKCLNP 60
                                                                                                                                                                                                                                                                                    903 PUTATIVE PORIN.
95689 MW; B55F57DE651ABFB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 68 AA; 7468 MW; 9B5E2A11865E56BF CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to WAP four-disulfide core domain 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Porcine uteroferrin-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                      31.3%; Score 102.5; DB 5;
44.1%; Pred. No. 2e-05;
tive 2; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AA
                                                                                                 PRINTS; PRO0003; 4DISULPHCORE.
ProDom; PD001224; WAP; 8.
SMART; SM00217; WAP; 17.
PROSITE; PS00317; 4_DISULFIDE_CORE; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002221; WAP.
Pfam; PF00095; Wap; 1.
PRINTS; PR000003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                           POTENTIAL.
EMBL; AF036160; AAC04762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M31216; AAA31136.1; -.
HSSP; O46655; 1CJH.
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.19
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
                           HSSP; P19957; 2REL.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                  903 AA;
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Best Local Similarity
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1-JUAR-2002 (TrEMSUrel. 20, Last annotation update)
DJ447F3.3.1 (Novel protein with MAP-type (Whey acidic protein)
'four-disulfide core' domains (1soform 1) (Hypothetical 23.9 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Dendrobranchiata, Penaeoidea,
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                                                                                                                         DB 4; Length 139;
                                                                                                                     31.0%; Score 101.5; DB 4; Length 41.5%; Pred. No. 4.5e-06; rive 7; Mismatches 14; Indels
                                         Strausberg R.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026014; AAH26014.1; -.
SEQUENCE 139 AA; 15081 MW; D8BEADC6D7B89FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Stavrides G.S., Huckle E.J., Deloukas P.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALD50348; CAC36106.1; -.
EMBL; ALS51713; CAC39444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lloyd D.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 AA; 23877 MW; 8BOAFE81DF83E8BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Putative antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 CPRVIRKQSCL---KRCITDKTCPGVKKCCTLGCNKSCVVP 66
                                                                                                                                                                                    16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 CPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.0%; Score 101.5; DB 4 ilarity 41.5%; Pred. No. 7.1e-06; Conservative 7; Mismatches 14
                                                                                                                                                                                                                                                                                             224 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00217; WAP; 4.
PROSITE; PS00317; 4_DISULFIDE_CORE; 4.
                                                                                                                                                                                                                                                                                                                         Created)
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INTETPO: IRR002221; WAP.
Pfam; PF00095; WAP, 4D1SULPHCORE.
PRINTS; PR00003; 4D1SULPHCORE.
ProDom; PD001224; WAP; 2.
                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17,
                                                                                                                                                  Matches 17; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
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es 17; Conserv
                                                                                                                                       Best Local Similarity
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               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                               TISSUE=TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                   DJ447F3.3.
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                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                           Q9BQP3
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                                                                                                                                                                                                                                                             RESULT 31
Q9BQP3
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1D Q
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                                                                                                                    "Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penaeus vannamei (Penoeid shrimp) (Buropean white shrimp).
Eukaryota, Metazoa, Arthropoda, Crustacea; Malacostraca;
Eumalacostraca, Eucarida, Decapoda, Dendrobranchiata, Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
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                                                                                                                                                                                                                                                                                                                                                                     97 AHEP-ETPVGTKPLDCPQVRPTCPRFHGPPTTCSNDYKCAGLDKCCFDRC 145
                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 163;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative antimicrobial peptide.
Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;
                                                                                                                                                                                                                                                                                                                                              1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=HEMOLYMPH;
Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard E.F., Warr G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC 49
                                                                                                                                                                                                                                                                           30.9%; Score 101; DB 5; Length 15
42.0%; Pred. No. 5.7e-06;
ive 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.9%; Score 101; DB 5; Length 16
42.0%; Pred. No. 6.1e-06;
iive 4; Mismatches 23; Indels
                                                                                                                                      shrimp.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                     EMBL; AF430073; AAL36892.1; -...
InterPro; IPR002221; WAP.
SMART; SM00217; WAP. I.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 151 AA; 15265 WW; ABAEBB8BE9E2IA7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF430071; AAL36890.1; -.
INCECPTO; IPR00222; WAP.
SMART; SM00217; WAP!, WAP.
PROSITE; PS0017; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 163 AA; 16118 MW; 21D45A5115044C35 CRC64;
                                                                  IISSUE=HEMOLYMPH;
Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson
Shepard E.F., Warr G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative antimicrobial peptide.
                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 42.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
Penaeidae; Litopenaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penaeidae; Litopenaeus.
                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                 NCBI_TaxID=6689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6689;
                                                                                                                                                                                                                                                                             Query Match
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O8WRP4
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Penaeidae; Litopenaeus.

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Query Match
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                                                                                                                          Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
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Eumalacostraca, Eucarida, Decapoda, Dendrobranchiata, Penaeoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AHEP-ETPVGÍKPLDCPQVRPTCPRFHGPPTTCSNDYKCAGLDKCCFDRC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 163;
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                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penaeus vannamei (Penoeid shrimp) (European white shrimp).
                                                                                  Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard E.F., Warr G.W.;
                                                                                                                                                                                                                                                                                                                     30.9%; Score 101; DB 5; Length 16
42.0%; Pred. No. 6.1e-06;
iive 4; Mismatches 23; Indels
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EMBL; AF430075; AAL36894.1; -.
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                                                                                                                                                                     (OCT-2001) to the EMBL/GenBank/DDBJ databases
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SWART; SMO217; WAP; 1
PROSITE; PS00117; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 163 AA; 16148 MW; 3C145A5108C445F5 CRC64;
                                                                                                                                                                                                                              SMARY; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 163 AA; 16207 MW; 67FFF8D210BE3CFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last
Putative antimicrobial peptide.
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                                                                                                                                                                                         EMBL; AF430072; AAL36891.1; -. InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                          Local Similarity 42.0%;
nes 21, Conservative
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NCBI_TaxID=6689;
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NCBI_TaxID=64468;
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                                        SEQUENCE FROM N.A.
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                                                                TISSUE=HEMOLYMPH;
NCBI_TaxID=6689;
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Matches
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Q8WRP1
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REDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamser G. Wortman J. R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Adgayani A.A. An H.-J., Andrews Pfannkoch C., Baldwin D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Backer B.P., Rhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Backer B.P., Rhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Backer B.P., Rhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Pleischmann W.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daviss P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
ROSIER C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Alostin D., Harvey D., Heiman T.J., Hernandez J.K., Houck J.,
RA Alostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Milshian N.V., Mobarty C., Norris J., Nosherson D.L.
RA Merkulov G., Milshian N.V., Mobarty C., Norris J., Puri V., Rese M.G.,
RA Reinert K., Remington K., Sampson M., Skupski M.P., Shith T.,
RA Spier B.C., Siden-Klamos I., Simpson M., Skupski M.P., Shith T.,
RA Spier B.C., Siden-Klamos I., Sungson M., Skupski M.P., Shith T.,
RA Spier B.C., Siden-Klamos I., Sungson M., Wang X.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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Bukaryote; Metazoa; Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                   Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC 49
                                                                     Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard E.F., Warr G.W.;
                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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es 21; Conserv
SEQUENCE FROM N.A.
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                                    TISSUE=HEMOLYMPH;
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NCBI_TaxID=7227;
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng K.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venrer J.C.;
I The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
I Science 287:2185-2195(2000).
REBL; AE003746; AAFS6243.1; -.
R HSSP; P19957; 2REL.
R Flyase; FBGn0039155; CG6173.
R InterPro; IPR003261; WaF.
R InterPro; IPR002221; WaF.
R Pfam; PF000941; fn3; 2.
R Pfam; PF00095; wap; 1.
R RANTY; SM00060; FN3; 1.
R SMART; SM00217; WAP: 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;

"Invertebrate homologs of the Kallmann syndrome gene.";

"Invertebrate homologs of the EMBL/GenBank/DDBJ databases.

EMBL; AF342988; AAL73340.1; -.

InterPro; IPR003961; FN III.

InterPro; IPR00201; MAP.

Pfam; PF00041; fn3; 2.

Pfam; PF00095; wap; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QEPVKGPVSTKPGSCPIILIRC-AMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.9%; Score 101; DB 5; Length 52:
41.1%; Pred. No. 1.9e-05;
tive 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00317; 4 DISULFIDE CORE; 1. SEQUENCE 522 AA; 59443 MW; BA0B12D3048F5709 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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'01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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SMART; SM00060; FN3; 2.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.9%
Best Local Similarity 41.1%
Matches 23, Conservative
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08WS92
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                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 EFLKYILSVKQGDCPAPEKASGFAAACV----ESCEADSECSGVKKCCSNGCGHTCQVP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EPVKGPVSTKPGSCPI----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93291868; PubMed=8513320;
Rugarli E.L., Lutz B., Kuratani S.C., Wawersik S., Borsani G.,
Ballabio A., Eichele G.,
"Expression pattern of the Kallmann syndrome gene in the olfactory system suggests a role in neuronal targeting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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د
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bingle C.D., Bingle L.; "Novel splice varients of the human HE4 gene are expressed in pulmonary epithelial cells."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF330260; AAL57486.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.6%; Score 100; DB 4; Length 76; 42.0%; Pred. No. 4e-06; Live 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 VSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VSDKEGSCPQVNINFPQLGLCRDQCQVDSQCPGQMKCCRNGCGKVSCVTP 74
                                                                                                                                                                                                                              Nat. Genet. 4:19-26 (1993).

HISSP: P19957; 2REL.

III terpro. 1PR003221; WAP.

Fam; PF00041; fn3; 3.

Pfam; PF00095; Wap. 1.

PRINTS; PR00003; 4D1SULPHCORE.

SMART; SM00060; FN3; 3.

SMART; SM00217; WAP. 1.

PROSITE; PS00317; WAP. 1.

SEQUENCE 675 AA; 76289 WW; 784393E4D603E2EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0003; 4DISULPHCORE.
SMART; SMO0217; MAR; 1.
SPOSITE; PSO0317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 76 AA; 8107 MW; A93BE754FDAC93©2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  30.7%; Score 100.5; DB 134.4%; Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AA.
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               Kallmann syndrome gene product.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.48;
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=PLACENTA;
MEDLINE=2108566; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 EFLKYILSVKQGDCP-----APEKASGFAAACFESCEADSECSGVKKCCSNGCGH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EPVKGPVSTKPGSCPIILIRCAMLNPPNR------CLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 99.5; DB 13; Length 674; 31.8%; Pred. No. 3.8e-05; cive 7; Mismatches 17; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00060; FN3; 3.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 674 AA; 76439 MW; 52ACDB45C75C0392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
101-JUAR-2002 (TrEMBLrel. 20, Last annotation update)
1600023A02Rik protein (WAP domain protein HE4).
                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                        Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 AA.
                                                674 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003961; FN III.
InterPro; IPR002221; WAP.
Pfam; PF00041; fn3; 3.
Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 31.8%;
les 21; Conservative
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                                                 PRELIMINARY;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                           NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 TCQVPK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ACFVPQ 57
                                                                                                                 KAL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                090369
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                        RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DAU7
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels 24; Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EPVKGPVSTKP------GSCPII----LIRCAMLNPPNRCLKDTDCPGIKKC 44
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"Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF309414; AAG25716.1; -.

HASP; 19957; ZREE.

InterPro; IRR00221; WAP.

FAMI, PR00095; wap: 1.

PRINTS; PR00095; wap: 1.

SWART; SM00217; WAP; 1.

PROSITE; PS00317; 4 DISULFIDE CORE; 1.

SWART; SM00217; 4 BISULFIDE CORE; 1.

SEQUENCE 421 AA; 38510 MW; 99698CF275C6FED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AK005519; BAB24094.1; --
EMBL, AF334269; AAL73189.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00003; 4DISULPHCORE.
SMART; SM0217; WAP; 2.
PROSITE; PS01317; 4 DISULFIDE CORE; 1.
SEQUENCE 174 AA; 18031 MW; 82484E28ED6FIE20 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ovarian fibroin-like substance-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 98; DB 11;
33.8%; Pred. No. 1.7e-05;
live 7; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 98; DB 13; 35.5%; Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, O46655; 1CJH.
MGD; MG11:1914951; 1600023A02Rik.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bingle C.D.; "Cloning of mouse HE4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL;
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RESULT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y., Kramerov A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D., Sieron A.L., Prockop D.J., Fessler J.H.; Papilin in development; a pericellular protein with a homology to the ADAMTS metalloproteinases."; Development 127:5475-5485 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                      5; Mismatches 19; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                       3 BPVKG-PVSTKPGSCPIILIRCAMLNPPN-----RCLKDTDCPGIKKCCEGSCGMACFV 55
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89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix protein papilin precursor.
PPN OR CG1540 OR CG18436.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 98; DB 5; Length 2174; 39.6%; Pred. No. 0.00019; tive 1; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1980 | F18411 | ANN | F1841 | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN | F1841 | ANN 
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SWART; SW00410; IG like; 1.
SWART; SW00131; KU; 3.
SWART; SW00209; TSP1; 7.
     Conservative
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches 22;
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12 KPGSCPIILIR---CAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56

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RA Adams M.D., Celniker S.E., 160 k.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., 160 k.A., Fashburner M., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Read Goorge R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N., Raddon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., Raddon R.C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G., Radlew R.M., Basu A., Baxendala J., Baytektaroglu L., Beasley E.M., Batllew R.M., Batllew R.M., Batllew R.M., Burler H.J., Andrews-Pfannkoch C., Baldwin D., Batllew R.M., Butler H., Cadieu E., Center A., Chandra I., Raddon K.Y., Buller R.A., Dahlke C., Davenport L.B., Davies P., Burtis R.C., Busam D.A., Buller C., Davenport L.B., Davies P., Burtis R.C., Busam D.A., Buller C., Davenport L.B., Davies P., Burtis R.C., Busam D.A., Buller C., Davenport L.B., Davies P., Batler R.A., Cong F. Corria C., Perraz C., Perraz C., Perraz C., Perraz C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Perras C., Pe
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Bukaryota; Metazoa; Arthropoda; Trachata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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1870 KPGECPALSANASGCA----RECYTDADCRGDNKCCSDGCGQLCVHP 1912
                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
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InterPro; IPR0031006; Ig_MHC.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
InterPro; IPR002221; WAP.
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FlyBase; FBgn0003137; Ppn.
InterPro; IPR000561; EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                       CG1540 protein.
PPN OR CG1540 OR CG18436.
                                                                                                                                                                                               PRELIMINARY;
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1. Biol. Chem. 272:32472-32481(1997).

1. Biol. Chem. 273:32472-32481(1997).

1. FUNCTION: PLASA A STRUCTURAL ROLE IN THE NACRE MATRIX FRAMEWORK OF THE SHELL. MAY ALSO PERFORM OTHER FUNCTIONS SUCH AS INTERACTING THE PROTEIN COMPONENTS OF THE MATRIX FROM DEGRADATION, AND CONFERRING ELASTIC RESILIENCE TO THE MATRIX SYNTHESIZED AND SECRETED SECRETED SECRETED SECRETED SECRETED COMAIN: THE PROTEIN CONTAINS THE MATLIAL CELLS.

1. DOMAIN: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH DOMAINS INTERSPERSED BY EIGHT PROLINE-RICH DOMAINS. A GLYCINE- AND SERINE-RICH DOMAINS INTERSPERSED BY EIGHT PROLINE-RICH DOMAINS. AND THESE ARE FOLLOWED BY A BASIC DOMAIN AND A C-TERMINAL DOMAIN THAT IS HIGHLY SIMILAR TO KNOWN PROTEASE

2. INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                                                                                                                                                                             L -> SVVPV (IN SHORT ISOFORM).
FNFKTMEDSGI -> VASPPLHPNAV (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 30.0%; Score 98; DB 5; Length 3060; Local Similarity 39.6%; Pred. No. 0.00026; les 19; Conservative 1; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2415 KPGECPALSANASGCA----RECYTDADCRGDNKCCSDGCGQLCVHP 2457
                                                                                                                                                                                                                                                                                                                                                                                                                           2855 3060 MISSING (IN SHORT ISOFORM).
3060 AA, 331579 MW, ACA31D3EE558C7C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KPGSCPIILIR---CAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
LUSTRIN A.
Pfam; PF00014; Kunitz_BPTI; 12.
Pfam; PF00090; tsp_1; 5.
Pfam; PF00090; tsp_1; 5.
Pfam; PF00095; wap; 1.
PRINTS; PR00759; MasicPrass.
ProDom; PD000222; Kunitz_BPTI; 12.
SMART; SM00131; KU; 12.
SMART; SM00210; TSP1; 7.
SMART; SM00211; Wap; 11.
PROSITE; PS00217; Wap; 11.
PROSITE; PS00280; BPTI KUNITZ_1; 11.
PROSITE; PS0029; BPTI KUNITZ_1; 11.
PROSITE; PS00029; BPTI KUNITZ_1; 12.
PROSITE; PS00029; BPTI KUNITZ_1; 13.
Alternative splicing; Immunoglobulin domain; Serine protease inhibitor.
VARSPLIC 2003 2803 1 .- SVVPV (IN SHO)
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InterPro; IPR002221; WAP.
InterPro; IPR002299; WR1/EB.
SWART; SW0003; 4DISULPHCORE.
SWART; SW00217; WAP; 1.
SWART; SW00217; WAP; 1.
SWART; SW00217; 4 DISULFIDE CORE; UNKNOWN_2.
Structural protein; Glycoprotein.
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TISSUE=MANTLE;
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97.5; DB 5; Length 1428; Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 KPGSCPIILIRCAMLNPPN-----RCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO022038; AAH02038.1; -.
HSSP; Q9N0L8; ITWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterProj IPR002221; WAP.
PEdm. PF001406; TRNA-Synt_le; 1.
PEfant, PF000095; WAP; 1.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SW00217; WAP; 1.
SEQUENCE. 225 AA; 24473 MW; BCCS254DEB3BS919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) similar to extracellular proteinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                               GLY/SER-RICH.
CYS-RICH.
ARG/LYS-RICH (BASIC).
TO LORICRIN.
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InterPro; IPR002221; WAP.
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01-JUN-2001 (TrEMBLrel. 17, Last seqn
01-MAR-2002 (TrEMBLrel. 20, Last ann
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Similarity 38.5%;
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1428 AA;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                Q9DEY0;
                                                                                                                                                                                                                                                                                                                                                     Q9DEY0
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                  01-MRR-2002 (TrEMBLrel. 20, Created)
01-MRR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative antimicrobial peptide.
Litopenaeus setiferus (white shrimp).
Litopenaeus Setiferus (white shrimp).
Eumalacostraca; Bucarida; Decapoda; Crustacea; Malacostraca;
Penaeidae; Litopenaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang Y.-S., Huang F.-L.;

"Transgluteminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF309416; AAG25718.1; -.

HisSP; O9NOLB; ITWP.

InterPro; IPR002395; Kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                 1; Mismatches 15; Indels 17;
                                                                                                                                         180 KPGACP-----KPPPRSFGTCDERCTGDGSCSGNMKCCSNGCGHACKPP 223
29.5%; Score 96.5; DB 11; Length 225; 37.7%; Pred. No. 3.4e-05;
                                                                                               12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 29.4%; Score 96; DB 5; Length 123; Local Similarity 41.7%; Pred. No. 2.2e-05; Loss 20; Conservative 4; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=HEMOLYMPH;
Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
Shepard E.F., Warr G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EP-EAPVGTKPLDCPQVRPTCPRFHGPPVTCSSDYKCGGVDKCCFDRC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shrimp.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF430077; AAL36896.1; -.
InterPro; IPR002221; WAP.
Pfam, PF00095; Wap; 1.
PROSIT: SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 123 AA; 13103 MW; 71249D81F6AD65B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ovarian fibroin-like substance-3.
                                                                                                                                                                                                                                                             PRT; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Query Match
Best Local Similarity 37.7%
Matches 20; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=64468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09DEX9;
                                                                                                                                                                                                                                                                                     OBWRN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DEX9
                                                                                                                                                                                                                                                             Q8WRN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                              RESULT 48
                                                                                                                                                                                                                                    Q8WRN9
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang Y.-S., Huang F.-L.;
"Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF309415; AAG25717.1; -...
                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                29.2%; Score 95.5; DB 13; Length 293; illarity 36.7%; Pred. No. 6e-05; Conservative 7; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.2%; Score 95.5; DB 13; Length 329; 43.4%; Pred. No. 6.7e-05; tive 3; Mismatches 16; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 PVSTKPGSCP----IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 pvsmkpdocpppkkipi--ca---kscvppdocpprokccprtrahacsep 85
                                                                                                                                                                                                                                                                                                     31 TVKPGQCPLPEMIPPCAA----SCFRDGQCPATQKCCPTTSGFACSEP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO10986; AAH10986.1; -.
InterPro; IPR002221; WAP.
Pfam; PF00095; Wap; 1.
PROSTIE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 74 AA; 7759 WW; 42BDCAD6830383D3 CRC64;
                                                                                                                                                                                                                                              10 STKPGSCPI - - ILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 1 1 2
SEQUENCE 329 AA; 31521 MW; 36467E1929CEC8A4 CRC64;
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SEQUENCE 293 AA; 27578 MW; ED8E220C4B6C2263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ovarian fibroin-like substance-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similar to extracellular proteinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                             Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00060; FN3; 3.
SMART; SM00217; WAP; 1.
Science 282:2012-2018(1998).
                                InterPro; IPR003961; FN III.
InterPro; IPR002221; WAP.
Pfam; PF00041; fn3; 3.
Pfam; PF00095; wap; 1.
        EMBL; Z81561; CAB04551.1; -. HSSP; Q9N0L8; 1TWP.
                                                                                                                                                               Best Local Similarity 34.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                   Q8WS94;
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                                                                                                                                                                                                                                                                                     08WS94
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Q8WS94
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QEPVKGPVSTKP-----GSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGS 48
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                17;
                                                                              29 KPGACP-----KPPPRSFGTCDEQCTGDGSCSGNMKCCSNGCGHACKPP 72
           Length 74;
                                                                                                                                                                                                                                                                                               Bingle C.D., Bingle L.;
Novel splice varients of the human HE4 gene are expressed
pulmonary epithelial cells.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                        12 KPGSCPIILIRCAMLNPPNR------CLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 4; Length 73;
Pred. No. 2.5e-05;
6; Mismatches 25; Indels
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 73 AA; 8120 MW; BDCFEECFA4FBBD59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                             Last sequence update)
Last annotation update)
         Query Match 28.9%; Score 94.5; DB 11; Best Local Similarity 37.7%; Pred. No. 2.2e-05; Matches 20; Conservative 1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 AA
                                                                                                                                                                                                   WAP domain containing protein HE4-V3
                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                           PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                            EMBL; AF330261; AAL37487.1; -. InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%;
ilarity 34.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 CG-MACFVP 56
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63 CGKVSCVTP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K03D10.1 protein.
                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K03D10.1
                                                                                                                                                      OBWXWO;
                                                                                                                                        OBWXWO
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062299
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Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;

"Invertebrate homologs of the Kallmann syndrome gene.";

"Invertebrate homologs of the EMBL/GenBank/DDBJ databases.

EMBL; AF342986; AAL73338.1; -.

InterPro; IPR003961; FN III.

InterPro; IPR00341; FN III.

Pfam; PF00041; fn3; 3.

Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                       Gaps
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Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                28.3%; Score 92.5; DB 5; Length 662; 34.0%; Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 KPGACPSVSNQSNYECSAL----CQMDGECPETQKCCSSGCSRQCLKPR 147
                                                                                                                                                                                                                                                                                                                                                                                                 65 KPGACPSVSNQSNYECSAL----CQMDGECPETQKCCSSGCSRQCLKPR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 KPGSCPIIL----IRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                    12 KPGSCPIIL----IRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
PRINTS; PR00003, 4DISULPHCORE.
SMART; SM00060; FN3; 1.
SMART; SM00217; WAP, 1.
SMART; SM00217; WAP, 1.
SEQUENCE, PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 662 AA, 74166 MW; 9199A76E8C9117B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 700 AA; 78584 MW; 2975913064E98IE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 AA
                                                                                                                                                                                                                                                                    6; Mismatches
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09-833799-13b.rspt

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OSWRPO;
                                         Q8WRP2
Q8WRP2;
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RESULT 57
                         Q8WRP2
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                                                     Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
Hardelin J.P., Petit C.;
RT "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT underlying X chromosome-linked Kallmann syndrome.";
Mech. Dev. 90:89-94 (2000).
REMBL; AF163311; AAF25780.1; -.
RICEPPO; IRRO02231; WAP.
RICEPPO; IRRO03361; WAP.
REMP: PRO0005; Wap; 1.
REMP: REMP: RO0005; Wap; 1.
REMP: RO0005; Wap; 1.
REMP: REMP: RO0005; Wap; 1.
REMP: REMP: RO0005; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 EFLRSVMVVKQGDCP-----PPERASGFAAACVEGCEEDGECSGQKKCCPNGCGH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20054095; PubMed=1058556;
Ardouin O., Legouin R., Fasano L., David-Watine B., Korn H.,
Hardelin J.P., Petit C.; Fasano L., David-Matine B., Korn H.,
Hardelin J.P., Petit C.; Fetit C.; Fetit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit C.; Petit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EPVKGPVSTKPGSCPIILIRCAMLNPPNR------CLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 KQGDCP-----PAQRASGFAAACVESCAQDRECSGVKKCCSNGCGHTCQSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KPGSCPIILIRCAMINPPNR------CLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%; Score 91.5; DB 13; Length 652; ilarity 30.3%; Pred. No. 0.00045; Conservative 6; Mismatches 19; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 91.5; DB 13; Length 633; 32.1%; Pred. No. 0.00044; ive 3; Mismatches 14; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SM00060; FN3; 3.
SWART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SEQUENCE 652 AA; 72581 MW; 07D6D12D35AA1160 CRC64;
                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00317, 4 DISULPIDE CORE, 1. SEQUENCE 633 AA, 70672 MW; DAC21803F8899E03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                              MEDLINE=20054095; PubMed=10585565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF163310; AAF25779.1; -. InterPro; IPR003961; FN III. InterPro; IPR002221; WAP. PF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 32.19
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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ses 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyprinidae; Danio.
NCBI_TaxID=7955;
                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , 162 TCQSPK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ACFVPQ 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9IAR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9IAR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 56
Q91AR4
ID Q91AR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustecea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Litopenaeus.
                                                                                                                                 Putative antimicrobial peptide.

Peraeus vannamei (Penoeid shrimp) (Buropean white shrimp).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Bucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 AHEP-ETPVGTKILDCPQVRPTCPRFHGPPTTCSNDYKCAGLDKCCFDRC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AHEP-ETPVGTKILDCPQVRPTCPRFHGPPTTCSNDYKCAGLDKCCFDRC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.8%; Score 91; DB 5; Length 169; 40.0%; Pred. No. 0.00014; ive 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%; Score 91; DB 5; Length 163; 40.0%; Pred. No. 0.00014; tive 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard E.F., Warr G.W.,
                                                                                                                                                                                                                                                                                                                                                                             Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard E.F., Marr G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF430076; AAL36895.1; -.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF430074; AAL36893.1; -. InterPro; IPR00221; WAP. PROSITE; PR00317; 4 DISULFIDE CORE; UNKNOWN 1. SEQUENCE 163 AA; 16134 MW; E8D4434815044C26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00317; 4 DISTLFIDE CORE; UNKNOWN 1.
SEQUENCE 169 AA; 16575 MW; 7F6E04EEAC88388E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                             (TrEMBLrel. 20, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 AA.
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                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative antimicrobial peptide.
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nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                  Penaeidae; Litopenaeus.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               TISSUE=HEMOLYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=HEMOLYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6689;
                                                                                                                                                                                                                                                                      NCBI_TaxID=6689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shrimp.";
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ID Q2
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HSSP; 046655; 1CJH.
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NON TER
SEQUENCE
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                                                                                Q9IAR5
Q9IAR5;
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                                    RESULT 61
                                                                D9IAR5
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                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J., Shepard B.F., Warr G.W., "Characterization of a putative antimicrobial peptide from penaeid
                                                                                                                                                                                                                                                                                                                                                                            Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR 2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Putative antimicrobial peptide.
Putative antimicrobial peptide.
Litopenaeus setiferus (white shrimp).
Eukaryota, Metazoa, Arthropoda, Crustacea; Malacostraca;
Eumalacostraca; Bucarida, Decapoda, Dendrobranchiata; Penaeoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 QPVRWPGPNAKPGSCPPSPVGAVGL--ASFCQSDFDCMGYQKCCITTAGYECTHP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.7%; Score 90.5; DB 5; Length 475; Best Local Similarity 38.2%; Pred. No. 0.00046; Matches 21; Conservative 7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                     Brooks H.;
Thesis (1997), Department of Biology, Imperial College of Strehnology and Medicine, University of London, London, U.K. EMBL; X78981; CAA55584.1; --
HSSP, P19957; ZREL.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.5%; Score 90; DB 5; Length 141; Best Local Similarity 38.9%; Pred. No. 0.00017; Matches 21; Conservative 3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shrimp.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF430079; AAL36898.1; -.
                                                                                                                                                                                                                                                               Drake L., Brooks H., Barker G.C., Bundy D.A.P.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002221; WAP.
SWART; SM0217; WAP;
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 141 AA; 14639 MW; FBDD7707548E8597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 AA; 50257 MW; E6785DED01EF1E65 CRC64;
                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-ANG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNU-2002 (TrEMBLrel. 21, Last annotation update)
Tt52 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0003; 4DISULPHCORE.
ProDom; PD001224; WAP; 4.
SMART; SM00217; WAP; 9.
PROSITE; PS00317; 4_DISULFIDE_CORE; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penaeidae, Litopenaeus.
NCBI_TaxID=64468;
                                                                                                                              Frichuris trichiura.
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                                                                                                                                                                                          NCBI_TaxID=36087;
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SEQUENCE
                                                                                                                                                                          Trichuris.
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Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
Hardelin J.P., Petit C.; Fasano L., David-Watine B., Korn H.,
Hardelin J.P., Petit C.; Fasano L.,
"Characterization of the two zebrafish orthologues of the KAL-1 gene
underlying X chromosome-linked Kallmann syndrome.";
Mech. Dev. 90:89-94(2000).
BMBL, AF163309; AAP25778.1;
InterPro; IPR00221; FN III.
InterPro; IPR00221; WAP.
Pfam; PF00041; fn3; 1.
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                                                                                                                                           Kall (Fragment).

Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
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Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodoncia; Sciurognathi; Muridae; Murinae; Mus.
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Hagiwara K., Kikuchi T., Endo Y., Huqun, Takahashi M., Xin X.,
Hagiwara K., Kikuchi T., Endo Y., Huqun, Takahashi M., Xin X.,
Hoshi S., Miki M., Incoka N., Tokue Y., Nukiwa T.;
"Mouse SWAMI (single WAP motif protein 1) gene.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF776974; AF86471.1; -.
EMBL; AF482009; AAL90747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.4%; Score 89.5; DB 13; Length 178; 31.0%; Pred. No. 0.00024; tive 3; Mismatches 16; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AA; 19950 MW; BD8192BD7B4072AA CRC64;
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Last annotation update)
                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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SMART; SM00060; FN3; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
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PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31033;
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16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
  TISSUE=OVARY
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Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;

"Invertebrate homologs of the Kallmann syndrome gene.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF342987; AAL73339.1; -.

InterPro; IPR003962; FnIII repeat.

InterPro; IPR0032221; WAF.

Pfam; PF00041; fn3; 1.

Pfam; PF00055; wap; 1.
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                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                 1;
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                                                                                                                                                               Query Match 26.8%; Score 87.5; DB 11; Length 80; Best Local Similarity 37.3%; Pred. No. 0.00021; Matches 19; Conservative 5; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                         26 KKNVFSKPGYCPEYRVPCPFVLIP-KCRRDKGCKDALKCCFFYCQMRCVDP 75
                                                                                                                                                                                                                                                              6 KGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 26.0%; Score 85; DB 5; Length 472; Local Similarity 30.8%; Pred. No. 0.0025; es 16; Conservative 5; Mismatches 17; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cortical granule protein with LDL-receptor-like repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00060; FN3; 2.
SMART; SM0217; WAP; 1.
PROSITE: PS00117; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 472 AA; 53942 MW; C80E59470A99DBBE CRC64;
                   Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 80 AA; 9237 MW; 9135647ED91F63ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                472 AA.
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01-NOV-1996 (TrEMBLrel. 01, Last serm
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PRINTS; PR00014; FNTYPEIII.
InterPro; IPR002221; WAP.
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Q26615;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2000 (TrEMBLrel. 21, Last annotation update)
Elafin-like protein II (SWAM2 protein).
Mus musculus (Wouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                          Wessel G.M.;
"A protein of the sea urchin cortical granules is targeted to the fertilization envelope and contains an LDL-receptor-like motif.";
Dev. Biol. 167:388-397(1995).
EMBL; U17377; AAA85106.1; -.
HSSP; Q07954; 1CR8.
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Hagiwara K., Kikuchi T., Endo Y., Takahashi M., Xin X., Hoshi S., Miki M., Inooka N., Tokue Y., Nukiwa T.,
"Mouse SWANZ (single WAP motif protein 2) gene.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%; Score 85; DB 5; Length 1142; 30.3%; Pred. No. 0.0059; Live 5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hagiwara K., Hoshi S., Takahashi M., Miki T., Nukiwa T.; "ELM-like proteins."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1142 AA; 127733 MW; A43043D2C023AB60 CRC64;
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Pfam; PF00095; Wap; 1.
SWART; SM00217; WAP.
PROSTITE; PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 85 AA; 9559 MW; 653546C95EF54AD7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 SMAKI; SMUULI, MAKI, MAKI, SMUULIDE CORE; 1. PROSITE, PS00317; 4 DISULFIDE CORE; 1. PROSITE; PS50068; LDLRA_1; 9. PROSITE; PS50068; LDLRA_2; 15.
                                                                                                                                                                                           Interproj IPR002172; LDL_recept_A.
Interproj IPR00221; WAP.
PEam; PF00057; Jal recept_a; 14.
PEam; PF00095; wap; 1.
PEANTS; PR00261; LDLRECEPTOR.
SWART; SM00192; LDLa; 14.
SWART; SM001217; WAP; 1.
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MEDLINE=95154582; PubMed=7851660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.003
Best Local Similarity 30.37
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Receptor NON TER 1142 1142 SEQUENCE 1142 AA; 12
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InterPro; IPR002221; WAP.
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Rhabditidae, Peloderinae, Caenorhabditis.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Wohldmann P., Bauer C., Gillam B.;
"The sequence of C. elegans cosmid F54E2.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
"Direct Submission.";
Submitted (UGG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF106579; AAC78198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 174 AA; 19998 MW; 64E86C37D9857C96 CRC64;
                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 20.0 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PGTCPTPTQLGYKCMVYTPISWCTTDQDCKG-KKCCPTGC 168
| : | | : | | | | | : | 32 CPPDYVRCIRQDDP-QCYSDNDCGDQEICCFWQCGFKCVLP 71
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                                                                    174 AA
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                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                    PRELIMINARY;
                                                                                                                                                  Caenorhabditis elegans.
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                                              RESULT 66
Q9TXK3
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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MEDLINE=98136158; PubMed=9468514;
Larsen M., Ressler S.J., Lu B., Gerdes M.J., McBride L., Dang T.D.,
Rowley D.R.;
"Molecular cloning and expression of ps20 growth inhibitor. A novel
WAP-type 'four-disulfide core' domain protein expressed in smooth
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MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                Query Match 24.9%; Score 81.5; DB 4; Length 102; Best Local Similarity 32.7%; Pred. No. 0.0017; Matches 17; Conservative 6; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                      25 VSGTGAEKTGVCPELQ---ADQNCTQECVSDSECADNLKCCSAGCATFCSLP 73
                                                                                                                                                                                                                                                                                                                     5 VKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
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J. Biol. Chem. 273:4574-4584(1998).
EMBL, AF037272; AAC40055.1; -.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
SMART; SM00217; WAP, 1.
PROSTIE; PS00317; WAP, 1.
SEQUENCE 212 AA; -23230 WW; 28B054DE9D8460A5 CRC64;
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PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00217; WaP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SEQUENCE 102 AA; 11043 MW; 36C13D09AADZEISE CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rhell D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Romstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M., Actinoich S., Hill D., Hofmann M., Hume D.A., Kamiga M., Lee N.H., Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Thencrional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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24.6%; Score 80.5; DB 11; Length 201;
Best Local Similarity 30.4%; Pred. No. 0.0045;
Matches 14; Conservative 6; Mismatches 15; Indels 11;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to WAP four-disulfide core domain 1 (Fragment).
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InterPro; IPR00221; WAP.
Pfam, PF00095; WAP; 1.
PROSITE; PS00317; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 201 AA; 22043 MW; 3D2E166752A4EEE9 CRC64;
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(TrEMBLrel. 16, Last sequence update)
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01'-MAR-2001 (
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Q9ESH5
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STRAIN=129/SVJ;
MEDINE=20424791; PubMed=10967136;
Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
Rowley D.R.;
                                                                                                                                                                                 "The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
                                                                                                                                                                                                                                                                                                                                                                     11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                       24.6%; Score 80.5; DB 11; Length 211; 30.4%; Pred. No. 0.0048; tive 6; Mismatches 15; Indels 11;
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STRAIN=BRISTOL N2;
Pauley A., Andrews S.;
"The sequence of C. elegans cosmid R12Al.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                           multiple cancers.";

Mamm. Genome 11:767-773(2000).

MBL; AF170446; AAG21086.1; J.

EMBL; AF1806221; WAP.

InterPro; IPR002221; WAP.

Ffam; PP00095; wap; 1.

SWART; SM00317; WAP; 1.

PROSITE; PS00317; A DISULFIDE CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                              8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                        61 PRTLPPGAC------QATRCQADSECPRHRRCCYNGCAYAC 95
01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Prostate stromal protein ps20.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequented)
01-MAR-2002 (TrEMBLrel. 20, Last annown typochetical 26.1 kDa protein.
R12A1.3.
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Pfam; PF00095; wap; 1.
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                                         Mus musculus (Mouse)
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Best Local Similarity
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                                                                                                           SEQUENCE FROM N.A.
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                                                                                  NCBI_TaxID=10090;
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MEDILNE=20424791; Pubmed=10967136;
Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
Rowley D.R.;
"The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-UTERUS;
ONG C.K., NG C.Y., Lim K.B., Chan T.W.M.G., Huynh H.;
"Molecular Cloning and Characterization of the Human PS20 protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                           Query Match 24.5%; Score 80; DB 5; Length 249; Best Local Similarity 40.5%; Pred. No. 0.0065; Matches 15; Conservative 7; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF302109; AAG15263.1; -.
InterPro; IPR002221; WAP.
Pfam; PF000095; wap; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SEQUENCE 168 AA; 18146 MW; 089AA8C5B0B9E1A0 CRC64;
ProDom; PD000222; Kunitz_BFTI; 1.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
PROSITE; PS00280; BFTI KUNITZ_1; 1.
PROSITE; PS50279; BFTI KUNITZ_1; 1.
Hypothetical protein; Serine protease inhibitor.
SEQUENCE 249 AA; 26084 MW; B7BC113CCFF2E1DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 PRILPPGACQAA------RCQADSECPRHRRCCYNGCAYAC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 16, Last sequence update) Ps20 WAP-type four-disulfide core domain protein. Hubence sapiens (Human).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                  81 INSKSGSCPRPLGISVFQDNTIGCWMDSNCPGIQKCC 117
                                                                                                                                                                                                                                9 VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCC 45
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Uterus."
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ461P17.11 (Novel protein with a WAP-type (Whey acidic protein)
four-disulfide core' domain and a kunitz/bovine pancreatic trypsin inhibitor domain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                      Ouery Match 24.3%; Score 79.5; DB 4; Length 220; Best Local Similarity 30.4%; Pred. No. 0.0068; Matches 14; Conservative 6; Mismatches 15; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QEP--VKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark L.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL011663; CAC36264.1; -...
HSSP; P05067; LAAP.
                                                                                                                                                                                                                                                 Mamm. Genome 11:767-773 (2000).

EMBL, AF169631; AAG16647.1; -.

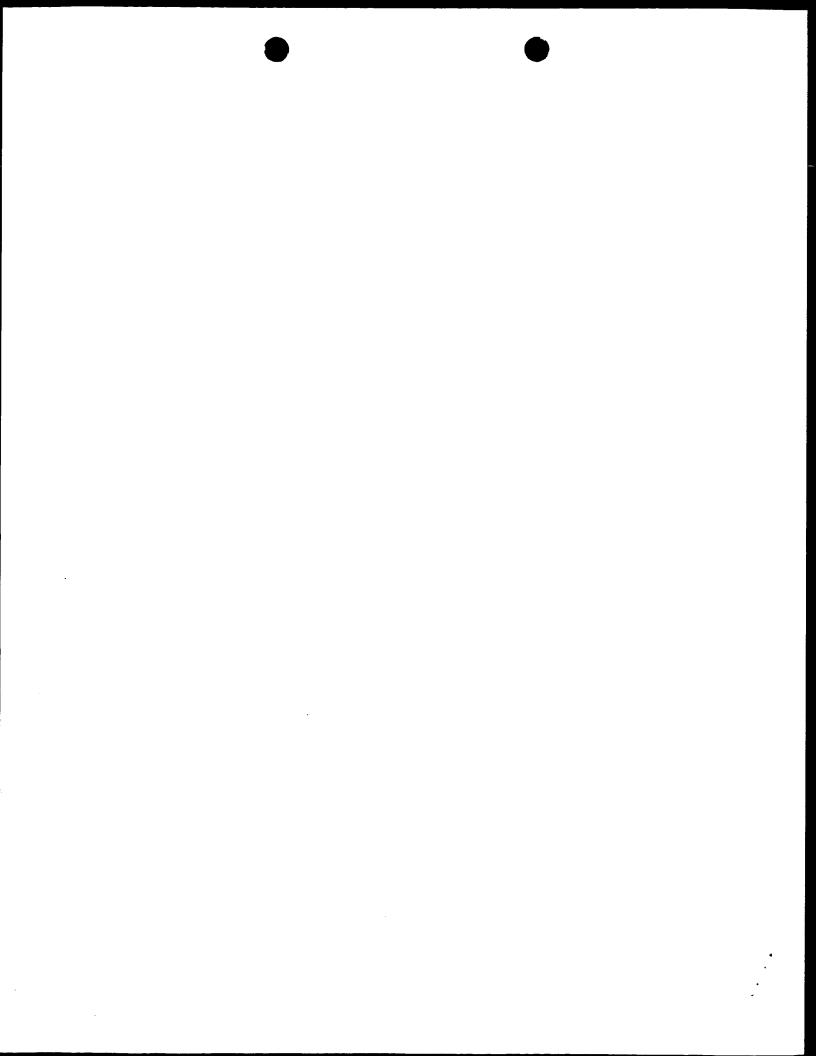
InterPro; IPR002221; WAP.

Pfam; PR00095; wap; 1.

SMART; SM00121; WAP; 1.

SMART; SM00317; 4 DISULFIDE CORE; 1.

SEQUENCE 220 AA; 24004 MW; 8098EB8449F88CBD CRC64;
                                                                                                                                                                                                                               8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
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SEQÜENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
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ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
Serine protease inhibitor.
NON_TER 131
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InterPro; IPR002221; WAP.
Pfam; PF00014; Kunitz_BPTI; 1.
Pfam; PF00095; wap; 1.
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multiple cancers.";
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ATPase inhibitor 3
trappin-6 - bovine
trappin-11 - hippo
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probable proteinas
hypothetical prote
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                                                  February 11, 2003, 08:36:01; Search time 46 Seconds (without alignments) 119.123 Million cell updates/sec
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                                                                                                       1 aqepvkgpvstkpgscpiil.....cpgikkccegscgmacfvpq
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 100 summaries
                                  OM protein - protein search, using sw model
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T32497
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JE0250
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JE0253
C33429
JE0252
JE0257
A36113
B35752
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A47222
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T23271
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S17982
A24178
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A, Residues: 1-139 <FUR>
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-117 <moi>A;Cross-references: GB:Z18538; NID:g28711; PIDN:CAA79223.1; PID:g28712
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A;Cross-references: GB:Z18538; NID:g28711; PIDN:CAA79223.1; PID:g28712
A;Title: Isolation of elafin and elastase-specific inhibitor (ESI) from bronchial secret A;Reference number: S20280; MUID:92162196; PMID:1536690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: JH0614
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Redow, O.; Schroeder, J.M.; Gregory, H.; Young, J.A.; Christophers, E.
J. Biol. Chem. 265, 14791-14795, 1990
J. Biol. Chem. 265, 14791-14795, 1990
A,Title: Blaffn: an elastase-specific inhibitor of human skin. Purification, characteriz
A;Reference number: A35800; MUID:90368643; PMID:2394696
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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: 71-78 <SAL>
B;Sallenave, J.M.; Ryle, A7.
Biol. Chem. Hoppe-Seyler 372, 13-21, 1991
A;Title: Purification and characterization of elastase-specific inhibitor. Sequence home
A;Reference number: S13455; MUID:91248412; PMID:2039600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A39522
A;Aolecule type: protein
A;Rosidues: 61-77 < W12>
R;Molhuizen, H.O.F.; Alkemade, H.A.C.; Zeeuwen, P.L.J.M.; de Jongh, G.J.; Wieringa, B.;
D. Biol. Chem. 268 120208-12032, 1993
A;Title: SKALP/elalin: an elastase inhibitor from cultured human keratinocytes. Purifica
A;Reference number: A46749; MUID:93280175; PMID:7685029
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A;Accession: IS1924
A;Status: preliminary; translated from GB/EWBL/DDBJ
                                                                                                                                                                                                              Alternate names: elastase inhibitor; proteinase inhibitor 3, skin-derived; skin-derive,
                                                                                                                                                                                                                                         C; Species: Homo sapiens (man)
C; Date: 17-Aug-1992 #text change 08-Oct-1999
C; Date: 17-Aug-1992 #text change 08-Oct-1999
C; Accession: JH6614; A35800; A39522; A46495; S20280; S13607; I51934
R; Saheki, T.; Ito, F.; Hagiwara, H.; Saito, Y.; Kuroki, J.; Tachibana, S.; Hirose, S. Biochem Biophys. Res. Commun. 185, 240-245, 1992
A; Title: Primary structure of the human elafin precursor preproclafin deduced from the A; Reference number: JH6614; MUID:92287100; PMID:1339270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 67.77. PG', 75-117 < WIE>
A; Moleci this sequence has been revised in reference A39522
B; Wiedow, O.; Schroeder, J.M.; Gregory, H.; Young, J.A.; Christophers, E. B. Diol. Chem. 256, 3356, 1991
A; Reference number: A39522
A; Contents: erratum
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A; Molecule type: DNA
A; Residues: 1-17 < RES>
A; Residues: 1-17 < RES>
A; Cross-references: GB:S58717; NID:g299840; PIDN:AAB26371.1; PID:g299841
C; Genetics:
A; Gene: GDB:P13
A; Gross-references: GDB:203940; OMIM:182257
A; map position: 20q12-20q13
A; Introns: 27/1
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F:1-25/Domain; signal sequence #status predicted <SIG>
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 70-90, 'CP', 93-94 <SA2>
R;Sallenave, J.M.; Silva, A.
Am. J. Respir. Cell Mol. Biol. 8, 439-445, 1993
ALIGNMENTS
                                                                                                                                                                           lafin precursor - human
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Cibate: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
Cipate: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
Cipatession: JBD0251
R;Furutani, Y:, Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S. B. Brothen: 124, 491-2502, 1998
A;Fulle: Evolution of the trappin multigene family in the suidae.
A;Reference number: JB0250; MUID:98391820; PMID:9722657
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C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C;Accession: JB0254
R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
J;Bichem: 124, 491-2502, 1998
A;Tile: Evolution of the trappin multigene family in the suidae.
A;Reference number: JB0250; MJID:983991820; PMID:9722657
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                                                                                                                                                                                                                                                                                                                                      61 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 117
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                                                                                                                                              Length 117;
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                                  F;61-117/Product: elafin #status experimental <MAT> F;72-117/Domain: antileukoproteinase repeat homology <ALP>
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F;94-139/Domain: antileukoproteinase repeat homology <ALP>
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F;26-60/Domain: propeptide #status predicted <PRO>
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A;Molecule type: protein
A;Residues: 127-187 <ARA>
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-187 < KU2>
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A; Residues: 1-181 <FUR>
A; Molecule type: mRNA
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N.Contains: ATPase inhibitor SPAI-1
C.Species: Sus scrofa domestica (domestic pig)
C.Species: 21-Reb-1997 #sequence revision 21-Feb-1997 #text_change 05-Nov-1999
C.Accession: 146650, 146651, B33429, A33429
R.Kuroki, J.; Hosoya, T.; Itakura, M.; Hirose, S.; Tamechika, I.; Yoshimoto, T.; Ghoneim J. Biol. Chem. 270, 22428-22433, 1995
A.Title: Cloning, characterization, and tissue distribution of porcine SPAI, a protein w A.Reference number: 146650; MUID:95403443; PMID:7673229
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R; Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S. J. Biochem. 124, 491-502, 1998
A; Title: Evolution of the trappin multigene family in the suidae.
A; Reference number: JE0250; MJID:98391820; PMID:9722657
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R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
                                      trappin-10 - collared peccary
C;Species: Tayassu tajacu (collared peccary)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Phacochoerus aethiopicus (wart hog)
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 201; DB 2; Length 153; Pred. No. 6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-207 «FUR»
A;Cross-references: DDBJ:AB003281
C;Superfamily: antileukoproteinase repeat homology
F;162-207/Domain: antileukoproteinase repeat homology «ALP»
                                                                                                                                                                                                                                                                                                                A;Cross-references: DDBJ:D50323
C;Superfamily: antileukoproteinase repeat homology
F;107-152/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.5%; Score 181.5; DB 2; Best Local Similarity 47.6%; Pred. No. 7.8e-12; Matches 30; Conservative 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6%
Matches 35; Conservative
                                                                                                                                                                                                                                        A, Accession: JE0256
A, Molecule type: mRNA
A, Residues: 1-153 <FUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trappin-1 - wart hog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JE0250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 YPK 207
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A,Cross-references: GB:D17755, NID:g1054614; PIDN:BAA04603.1; PID:g1054617
R,Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.
Biochem. Biophys. Res. Commun. 164, 496-502, 1989
A,Title: Novel peptide inhibitor (SPA1) of Na(+), K(+)-ATPase from porcine intestine. A,Reference number: A33429; MUID:90026425; PMID:2553020
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R,Furutani, Y, Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, J. Biochem. 124, 491-502, 1998
J. Biochem. 124, 491-502, 1998
A,Title: Evolution of the trappin multigene family in the suidae.
A,Reference number: JE0250; MUID:98391820; PMID:9722657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPase inhibitor 3 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Peb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Feb-1997
C;Accession: C34429
R;Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Species: Sus scrofa domestica (domestic pig)
C,Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: antileukoproteinase repeat homology
C.Keywords: ATPase inhibitor
F;127-187/Product: ATPase inhibitor SPAI-2 #status experimental <MA2>
F:139-187/Product: ATPase inhibitor SPAI-1 #status experimental <MA1>
F;142-187/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
A,Residues: 1-187 <KUR>
A,Cross-references: GB:D17753; NID:g1054611; PID:g1054612
A,Accession: 146651
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                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Note: this peptide has four disulfide bonds A,Accession: A33429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: duodenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 139-187 <AR2>
A;Experimental source: duodenum
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Matches 31; Conservative
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antileukoproteinase 1 precursor [validated] - human
N;Alternate names: elastase inhibitor; HUSI-1; mucus proteinase inhibitor; secretory leu
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                    A,Title: Novel peptide inhibitor (6PAI) of Na(+), K(+)-ATPase from porcine intestine. A,Reference number: A33429; MUD:90026425; PMID:2553020
A,Scatus: preliminary
A,Molecule type: protein
A,Residues: 1-61 < ARA>
C,Superfamily: antileukoproteinase repeat homology
C,Keywords: ATPase inhibitor
F;16-61/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C;Accession: JE0252
B;Furutani, Y; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S. J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
                                                                                                                                                                                                                                                                                                                                                                  1;
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R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S. J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
A;Accession: JE0257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AQPAVPGRFLLSKRGHCPGILFRCPLGNPSNKCWRDYDCPGVKKCCEGFCGKDCLYPK
                                                                                                                                                                                                                                                                                                                                                                                                                       1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                        52.4%; Score 171.5; DB 2; Length 61; 53.4%; Pred. No. 3.4e-11; tive 7; Mismatches 19; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%; Score 170; DB 2; Length 96;
45.5%; Pred. No. 6.8e-11;
tive 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-180 cFUR>
A,Cross-references: DDBJ:D83668
C,Superfamily: antileukoproteinase repeat homology
F;135-180/Domain: antileukoproteinase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;51-96/Domain: antileukoproteinase repeat homology <ALP>
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A,Residues: 1-96 <-PUR>
A,Cross-references: DDBJ:AB003283
C;Superfamily: antileukoproteinase repeat homology
Biochem. Biophys. Res. Commun. 164, 496-502, 1989
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Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                  31; Conservative
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                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trappin-6 - bovine
                                                                                                                                                                                                                                                                                                           Query Match
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antileukoproteinase precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Mar-1991 #sequence_revision 13-Jan-1993 #text_change 16-Jul-1999
C;Accession: A36113; A49198
R;Farmer, S.J.; Fliss, A.E.; Simmen, R.C.M.
A). Endocrinol. 4, 1095-1104, 1990
A;Title: Complementary DNA cloning and regulation of expression of the messenger RNA ence
A;Reference number: A36113; MUID:91155942; PMID:2293019
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C;Species: Cavia porcellus (guinea pig)
C;Accession: B35752
R;Coronel, C.E.; San Agustin, J.; Lardy, H.A.
B;Coronel, C.E.; San Agustin, J.; Lardy, H.A.
A;Title: Purification and Structure of caltrin-like proteins from seminal vesicle of the A;Reference number: A35752; MUID:90216715; PMID:2324101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-115 <FAR>
A;Cross-references: GB:M57446; NID:g164319; PIDN:AAA63446.1; PID:g164320
A;Cross-references: GB:M57446; NID:g164319; PIDN:AAA63446.1; PID:g164320
A;Note: the authors translated the codon GCT for residue 52 as Gly
R;Simmen, R.C.; Michel, F.J.; Fliss, A.E.; Smith, L.C.; Fliss, M.F.
Endocrinology 130, 1957-1965, 1992
A;Title: Ontogeny, immunocytochemical localization, and biochemical properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Noče: sequence extracted from NCBI backbone (NCBIP:89471)
C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;14-59/Domain: antileukoproteinase repeat homology <ALPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
125 ODPVKVPFLAAEGACPKIWIECSTLNPPKRCLRDAQCPRNKNCCPASCGKIC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ITNPVKVKPGKCPVVYGQCMMLNPPNHCKTDSQCLGDLKCCKSMCGKVCLTP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S GQAINRPGSCPRVMIYCPARHPPNKCTSDYDCPKPQKCCPGYCGKQCYQPE 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%; Score 165; DB 2; Length 11 48.1%; Pred. No. 2.6e-10; tive 6; Mismatches 21; Indels
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A;Residues: 1-55 <COR>
C;Superfamily: antileukoproteinase repeat homology
F;10-55/Domain: antileukoproteinase repeat homology <ALP>
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A;Status: preliminary
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A;Residues: 26-34;99-106;108-116;123-132 <BOU>
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Best Local Similarity 38.6'
Matches 32, Conservative
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mNNA
A; Molecule type: mNNA
A; Cross-references: GB:X04470; NID:g28638; PIDN:CAA28158.1; PID:g28639
B; Thompson, R.C.; Ohlsson, K.
B; Thompson, R.C.; Ohlsson, K.
A; Macline: Isolation, properties, and complete amino acid sequence of human secretory leuk
A; Reference number: A25890; MUID:86313644; PMID:3462719
A; Accession: A25890
A; Molecule type: protein
A; Residues: 26-132 cTHO
A; Molecule type: THO
A; Molecule type: Arhold
A; Molecule type: Arhold
A; Molecule type: Muidedenmann, K.; Machleidt, W.; Heinzel, R.; App
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A;Title: Oxidized mucus proteinase inhibitor: a fairly potent neutrophil elastase inhibi
A;Reference number: S50026; MUID:95031986; PMID:7945266
                                                                                                                                                                                                                                                                         Ajaccession: A25541
Ajmolecule type: DNA; mRNA
Ajmolecule type: DNA; mRNA
Ajmolecule type: DNA; mRNA
Ajmolecule type: DNA; mRNA
Ajmolecule: 1-132 sSTE>
Ajcross-references: GB:X04502; NID:g36485; PIDN:CAA28187.1; PID:g758101
R;Heinzel, R.; Appelhans, H.; Gassen, G.; Seemuller, U.; Machleidt, W.; Fritz, H.; Steff
R;Heinzel, R.; Appelhans, H.; Gassen, G.; Seemuller, U.; Machleidt, W.; Fritz, H.; Steff
AjTitle: Molecular cloning and expression of cDNA for human antileukoprotease from cervi
A;Reference number: A25007; MUID:87030258; PMID:3533531
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A;Title: The acid-stable proteinase inhibitor of human mucous secretions (HUSI-I, antile o whey proteins and Red sea turtle proteinase inhibitor.
A;Reference number: A01226; MUID:86164996; PMID:3485543
                             C;Date: 13. Aug-1986 #sequence revision 07-Jul-1995 #text change 08-Dec-2000 C;Accession: A25541; A25007; A25890; A01226; B01226; S13455; I55560; S14330; S21664; S56 R;Stetler, G.; Brewer, M.T.; Thompson, R.C. Nucleic Acids Res. 14, 7883-7896, 1986 A;Pitle: Isolation and sequence of a human gene encoding a potent inhibitor of leukocyte A;Reference number: A25541; MUID:87040761; PMID:3640338
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Biol. Chem. Hoppe-Seyler 372, 13-21, 1991
A;Title: Purification and characterization of elastase-specific inhibitor. Sequence homo
A;Reference number: S13455; MUID:91248412; PMID:2039600
A;Accession: S13455
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A,Residues: 26-52 <8h.>
R;Abe, T.; Kobayashi, N.; Yoshimura, K.; Trapnell, B.C.; Kim, H.; Hubbard, R.C.; Brewer,
J. Clin. Invest. 87, 2207-2215, 1991
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A,Residues: 26-34, X',36-42, X',44-50, XE',53-55;103-104, X',106-107 <BOE>
R,Radrews, J.L.; Melrose, J.; Ghosh, P.
Biol. Chem. Hoppe-Seyler 373, 111-118, 1992
A;Tile: A comparative study of the low-molecular mass serine proteinase inhibitors of A;Reference number: S21664; MUID:92265184; PMID:1886451
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Biochem, J. 274, 269-273, 1991
Ajitle: Purification of a serine-proteinase inhibitor from human articular cartilage.
A;Reference number: S14330; MUID:91158717; PMID:2001242
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R;Boudier, C.; Bieth, J.G.
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A;Molecule type: DNA
A;Residues: 1-26 <RES>
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A Residues: 26-132 <SEE>
A; Accession: B01226
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F;85-130/Domain: antileukoproteinase repeat homology <ALP2>
F;35-64,43-68,51-63,57-72,89-118,96-122,105-117,111-126/Disulfide bonds: #status predicte
F;45/Inhibitory site: Arg (trypsin) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status absent
F;89/Binding site: Leu, Met (elastase, chymotrypsin) #status predicted
C;Comment: This protein contains a four-disulfide core, a three-dimensional folding parture is also found in the related whey acidic proteins and chelonianin.

C;Comment: The sources of this protein include saliva, seminal plasma, and glandular tiss C;Comment: Human mucous fluids contain acid-stable proteinase inhibitors with strong affienchorceinases suggest that these inhibitors are encoded by a single gene expressed in
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R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, J. Blochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MÜID:98391820; PMID:9722657
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T3249.
R;Geisel, C.; Srellyes, L.
submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Sus_scrofa domestica (domestic pig)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
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A,Gene: GDB:SLPI; HUSI-I
A,Cross-references: GDB:9316429, OMIM:107285
A;Cross-references: GDB:9316429, OMIM:107285
C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
C;Keywords: duplication; glycoprotein; serine proteinase inhibitor
E;1-25,Domain: signal sequence #status predicted <SLS.
F;26-132/Product: antileukoproteinase 1 #status experimental <MAT>
E;31-76/Domain: antileukoproteinase repeat homology <ALP!>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 143; DB 1;
Pred. No. 5.4e-08;
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A;Accession: T3249:
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2150 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:D50322
C;Superfamily: antileukoproteinase repeat homology
F;70-114/Domain: antileukoproteinaso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
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Sun Feb 16 09:13:32 2003

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Cancerstrin, 27,77, Ramshaw, 11.A.; Kefford, R.F.
R.Dear, R.S. 48, 5203-5209, 1988
A;Title: Differential expression of a novel gene, WDNM1, in nonmetastatic rat mammary ade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 176, 247-254, 1991
A;Title: The WDNM1 gene product is a novel member of the 'four-disulphide core' family of
A:Reference number: JH0390; MUID:91207400; PMID:2018519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Gallus gallus (chicken)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: B47222; A47394; 536170
R;Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.; Mornow, J.P Genomics 17, 516-518, 1993
A;Title: Characterization of the chicken and quail homologues of the human gene responsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIE:137996)
R;Legouis, R.; Lievre, C.A.; Leibovici, M.; Lapointe, F.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 2461-2465, 1993
A;Title: Expression of the KAL gene in multiple neuronal sites during chicken developmen A;Reference number: A47394; MUID:93211991; PMID:8460158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 81-152, 'P',154-237 <LE2>
A; Residues: 81-152, 'P',154-237 <LE2>
A; Experimental Source: embryo, olfactory bulb
A; Note: sequence extracted from NCB1 backbone (NCBIN:128286, NCBIP:128287)
B; Rugarli, E.I.; Lutz, B.; Kuratani, S.C.; Wawersik, S.; Borsani, G.; Ballabio, A.; Eich
R; Rugarli, E.I.; Lutz, B.; Kuratani, S.C.; Wawersik, S.; Borsani, G.; Ballabio, A.; Eich
R; Rugarli, E.Y.; 19-26, 1993
A; Title: Expression pattern of the Kallmann syndrome gene in the olfactory system sugges
A; Reference number: 336170; MUID:93291868; PMID:8513320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
                                                                                                 WDNM1 protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_charge 05-Nov-1999
C;Accession: S07807; JH0390
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A;Cross-references: GB:Ll2144; NID:g406510; PIDN:AAA51435.1; PID:g406511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: EMBL:X13309; NID:g57500; PIDN:CAA31688.1; PID:g57501
A,Experimental source: thymus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 KPGKCP-----KNPPRSIGTCVELCSGDOSCPNIOKCCSNGCGHVCKSP 66
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A;Accession: S07807
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C,Superfamily: antileukoproteinase repeat homology
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C;Superfamily: antileukoproteinase repeat homology
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R;Dear, T.N.; Kefford, R.F.
Biochem. Biophys. Res. Commun. 176, 247-254, 1991
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A;Residues: 'MVR',5-528,'H',530-676 <RUG>
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A; Residues: 1-68 < DEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 9-68 <DE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mily actual process in precision 17-dan-1983 #text_change 21-Jul-2000 (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Spacession: A93920, A94340; Appella, E.; Qasba, P.K. Procession: A93920, A94370; Appella, E.; Qasba, P.K. Procession: A93920; MUD:82275050; PMID:6955785 (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appella) (Appe
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A; Residues: 1-3, 'S', 5-34, 'S', 36-38,'F', 40-67,'S', 69-115,'K', 117-128,'K', 130-133,'I', 135-
A; Residues: 1-3, 'S', 5-34,'S', 36-38,'F', 40-67,'S', 69-115,'K', 117-128,'K', 130-133,'I', 135-
A; Cross-references: GB: X01153; NID: 1957492; PIDN: CAA25600.2; PID: 195679681
C; Comment: Whey acidic protein and the neurophysius resemble each other in the number an otherwise there is little detectable similarity between these proteins.
C; Comment: This is one of the major protein components in the milk whey; although its fu cyclencities in hibitory function.
C; Genetics:
A; Introns: 30/1; 75/1; 129/1
C; Superfamily: antileuvoproteinase; antileuvoproteinase repeat homology
C; Keywords: duplication; milk; phosphoprotein; protein ase inhibitor
F; 1-19/Domain: signal sequence #status predicted <SIG>F; 0-197/Product: whey acidic protein #status predicted <MAT>F; 0-137/Product: whey acidic protein #status predicted <AMT>F; 0-137/Product: whey acidic protein #status predicted <AMT>F; 0-137/Products Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Applications Appl
                                                                                                                                                                                                  A;Map position: 4
A;Introns: 242/1; 306/1; 340/3; 485/1; 545/1; 736/2; 791/1; 829/1; 886/3; 942/1; 1079/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;79-127/Domain: antileukoproteinase repeat homology <ALP2>
F;34-61,48-65,48-60,54-69,83-115,96-119,102-114,108-123/Disulfide bonds: #status predict
F;39,40,103/Binding site: phosphate (Ser) (covalent) #status predicted
F;50/Binding site: phosphate (Thr) (covalent) #status predicted
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A; Cross-references: EMBL; AF036687; PIDN: AAB88311.1; GSPDB: GN00022; CESP: C08G9.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1347 PVSPAPGKLGTCPKLLI-----NPGCTEQCSQDSDCHGFLKCCQASCGTMCSAPR 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PVSTKP---GSCPIILIRCAMLNP--PNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                               Length 2150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
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                                                A, Experimental source: strain Bristol N2; clone C08G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%; Score 103; DB 1;
38.3%; Pred. No. 0.00077;
tive 5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                    Score 117; DB 2;
Pred, No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acidic protein precursor - rat
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                 A; Gene: CESP: C08G9.2
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C;Accession: S61553; 149390
R;Morrison, B.W.; Leder, P.
Orocgone 9, 3417-3426, 1994
A;Title: neu and ras initiate murine mammary tumors that share genetic markers generally A;Reference number: 148271; MUID:95060797; PMID:7970700
                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S22454
R;Kirchhoff, C; Habben, I; Ivell, R.; Krull, N.
Ridichhoff, C; Habben, I; Ivell, R.; Krull, N.
R;Kirchhoff, C; Habben, I; Ivell, R.; Krull, N.
A;Title: A major human epidid/ymis-specific cDNA encodes a protein with sequence homology A;Reference number: S25454; MUID:92153963; PMID:1686187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Superfamily: antileukoproteinase repeat homology
C.Keywords: extracellular protein; proteinase inhibitor
F.1-22.Domain: signal sequence #status predicted <SIG.
F.23-74/Product: probable proteinase inhibitor wdmml #status predicted <MAT>
F.29-73/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA; mRNA
A;Residues: 1-74 <MOR>
A;Cross-references: EMBL:X93037; NID:g1085069; PIDN:CAA63605.1; PID:g1085070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein K03D10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.Alternate names: WDNM1 protein
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                   epididymis-specific four-disulfide core protein HE4 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-125 <KIR>
A;Cross-references: EMBL:X63187; NID:g32050; PIDN:CAA44869.1; PID:g32051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: 20q12-20q13.2
C,Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;32-74/Domain: antileukoproteinase repeat homology <ALP1>
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12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 KPGACP-----KPPPRSFGTCDERCTGDGSCSGNMKCCSNGCGHACKPP
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47.6%; Pred. No. 0.003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;77-123/Domain: antileukoproteinase repeat homology <ALP2>
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Matches 20; Conservative
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T23271
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R;Shen, X.; Belcher, A.M.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.
J. Biol. Chem. 272, 32472-32481, 1997
J. Biol. Chem. 272, 32472-32481, 1997
J. Fitle: Molecular cloning and characterization of lustrin A, a matrix protein from shell A;Reference number: Z16496; MUID:98070424; PMID:9405458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cjacces at replay my advance restance of the control of the human gene responsion: A4722 Cjacces and A4722 Cjacces and advance of the chicken and quail homologues of the human gene responsion: A7 incles characterization of the chicken and quail homologues of the human gene responsion of A7 incles characterization of the chicken and quail homologues of the human gene responsion A7 incles characterization of the chicken and quail homologues of the human gene responsion A7 incles included in A7222 Muld. 9410957; PMID: 9406507 A; Accession: A4722 A; Accession: A4722 A; Accession: A4722 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; Accession: A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A; A7222 A
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A;Cross-references: EMBL:AF023459; NID:g2723361; PIDN:AAB95154.1; PID:g2723362
A;Experimental source: Lissue type mantle (shell and pearl nacre); cell type pallial
C;Superfamily: antileukoproteinase repeat homology
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C;Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 19-Feb-1999
C;Accession: A47222
R;Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Haliotis rufescens (California red abalone)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                  116 EFLKYILSVKQGDCPAPEKASGFAAACV----ESCEADSECSGVKKCCSNGCGHTCQVP 170
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                                                                                                                                                                                                                                                                     3 EPVKGPVSTKPGSCPI-----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                                                                                              DB 2; Length 676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%; Score 99.5; DB 2; Length 674; 31.8%; Pred. No. 0.006; Live 7; Mismatches 17; Indels 2
                                                                                                                                                                               23; Indels
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             F;125-171/Domain: antileukoproteinase repeat homology <ALP>
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                                                               30.7%; Score 100.5; DB 2 Best Local Similarity 34.4%; Pred. No. 0.0047; Matches 21; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 97.5; 38.5%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kallmann syndrome protein homolog KAL - quail
C.Species: Phasianidae qen. sp. (quail)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lustrin A - California red abalone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 TCOVPK 170
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Query Match Matches

RESULT 20

ò a

ò

ò

7

Gaps

5

Gaps

Gaps

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Miney acidic protein - Arabian camel
C;Species Camelus dromedarius (Arabian camel)
C;Species Camelus dromedarius (Arabian camel)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Aug-1997
C;Accession: A24178
R;Beg, O.U.; von Bahr-Lindstrom, H.; Zaidi, Z.H.; Jornvall, H.
Eur. J. Biochem. 159, 195-201, 1986
A;Title: A camel milk whey protein rich in half-cystine. Primary structure, assessment of A;Reference number: A24178; MUID:86300719; PMID:3743571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epididymis-specific four-disulfide core protein CE4 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 24-Oct-2000
C;Accession: IS4768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Trichuris trichiura
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-117 <BRO
C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;9-54/Domain: antileukoproteinase repeat homology <ALP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 EPV----LKDGRCPWVQTPLTAKHCLEKNDCSRDDQCEGNKKCCFSSCAMRCLDP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EPVKGPVSTKPGSCPIIL -- IRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 QPVRWPGPNAKPGSCPPSPVGAVGL--ASFCQSDFDCMGYQKCCITTAGYECTHP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 BPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                      130 KOGDCPAPEKASGFAAACV----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176
                                                                                                                                                                                                                28.3%; Score 92.5; DB 2; Length 680; 34.6%; Pred. No. 0.032; trive 3; Mismatches 20; Indels 11
                                                                                                                                                                                                                                                                                                                                                      12 KPGSCPI-----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.7%; Score 90.5; DB 2; Length 117; 37.5%; Pred. No. 0.013; tive 3; Mismatches 25; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.7%; Score 90.5; DB 2; Length 4 38.2%; Pred. No. 0.039; Live 7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X78981; NID:g520892; PID:g520893
C;Superfamily: antileukoproteinase repeat homology <ALP1-
F;131-174/Domain: antileukoproteinase repeat homology <ALP1-
F;232-275/Domain: antileukoproteinase repeat homology <ALP1-
A;Gene: GDB:KAL1; KAL
A;Cross-references: GDB:120116; OMIM:308700
A;Map position: Xp22.32-Xp22.32
C;Superfamily: antileukoproteinase repeat homology
F;130-176/Domain: antileukoproteinase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;64-111/Domain: antileukoproteinase repeat homology <ALP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Drake, L.; Brooks, H.; Barker, G.C.; Bundy, D.A.P. submitted to the EMBL Data Library, April 1994
A;Reference number: S47040
A;Accession: S47040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene Tt52 protein - Trichuris trichiura (fragment)
                                                                                                                                                                                                                                                 Best Local Similarity 34.6
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
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Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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A;Residues: 1-478 <DRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S47040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40392 #sequence_revision 24-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40392 #sequence_revision 24-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40392 #sequence_revision 3.; Wunderle, V.
G: Weissenbach, J. 1991
A;Title: The candidate gene for the X-linked Kallmann syndrome encodes a protein related A;Reference number: A40351; MUID:92005720; PMID:1913827
A;Accession: A40351
A;Status: preliminary
A;Molecule type: mRMA
A;Residues: 1-679 < LEG>A;Accession: A6085; NID:9237595; PIDN:AAB20108.1; PID:9237597
C;Genetics: GDB:120116; OMIM:308700
A;Genetics: GDB:120116; OMIM:308700
A;Map position: Xp22.32-Xp22.32
C;Superfamily: antileukoproteinase repeat homology
F;129-175/Domain: antileukoproteinase repeat homology
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Xallmann syndrome protein KALIG-1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
R;Franco, B.; Gaioli, S.; Pragliola, A.; Incerti, B.; Bardoni, B.; Tonlorenzi, R.; Carrc Nature 353, 529-536, 1991
A;Reference number: S17982; MUD:92018217; PMID:1922361
A;Accession: S17982
A;Accession: S17982
A;Accession: S17982
A;Accession: S17982
A;Residuale type: mRNA
A;Residuale type: mRNA
A;Residuale type: mRNA
A;Cxoss-references: EMBL:X60299; NID:934024; PIDN:CAA42841.1; PID:934025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                             A;Reference number: Z19719
A;Accession: T22271
A;Accession: T22271
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-662 <WIL>
A;Coss-references: RMBL:Z81561; PIDN:CAB04551.1; GSPDB:GN00019; CESP:K03D10.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.3%; Score 92.5; DB 2; Length 662; 34.0%; Pred. No. 0.031; tive 6; Mismatches 18; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KPGSCPI-----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KPGACPSVSNQSNYECSAL----CQMDGECPETQKCCSSGCSRQCLKPR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 KPGSCPIIL ---IRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                        A,Gene: CESP:K03D10.1
A,Map position: 1
A:Introns: 23/3; 78/3; 264/3; 597/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 34.0%
les 17; Conservative
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Matches 18; Conservative
   C; Accession: T23271
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A; Redidues: 1-134 cHENA
A; Redidues: 1-134 cHENA
A; Redidues: 1-134 cHENA
A; Note: the cDNA codons given for residues 1 (AGT) and 63 (CGT) are inconsisten
A; Note: the cDNA codons given for residues 1 (AGT) and 63 (CGT) are inconsisten
A; Note: they actidic protein and the neurophysins resemble each other in the number and pervise there is little detectable similarity between these proteins
B; Piletz, J.E.; Heinlen, M.; Ganschow, R.E.
A; Filetz, J.E.; Heinlen, M.; Ganschow, R.E.
A; Title: Biochemical characterization of a novel whey protein from murine milk.
A; Reference number: A92296; MUID:82052974; PMID:6975276
A; Contents: annotation; composition of tryptic peptides; strain YBR, variant
A; Note: the variant form appears to have one less Cys and one more Arg
A; Note: the variant form appears to have one less Cys and one more Arg
A; Note: the variant form appears to lavie on less Cys and one more Arg
A; Campbell, S.M.; Rosen, J.M.; Hennighausen, L.G.; Strech-Jurk, U.; Sippel, A.E.
A; Title: Comparison of the whey acidic protein genes of the rat and mouse.
A; Reference number: A94701; MUID:85062841; PMID:6095207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1,'S,'3:34,'Q',36-62,'V',64-86,'S',88-99,'K',101-134 <CAM>
A;Residues: 1,'S,'3:34,'Q',36-62,'V',64-86,'S',88-99,'K',101-134 <CAM>
A;Cross-references: GB:XO1157; NID:g55423; PIDN:CAA25604.1; PID:g1213616
C;Comment: This is one of the major protein components in the milk whey; although its fur described, inhibitory function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hennighausen, L.G.; Sippel, A.E.
Nucleic Acids Res. 10, 2677-2684, 1982
Nucleic Acids Res. 10, 2677-2684, 1982
A;Title: Mouse whey acidic protein is a novel member of the family of 'four-disulfide cos A;Reference number: A93423; MUID:82196900; PMID:6896234
A;Accession: A93423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N,Aiternate names: BIP
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: S01286; S12586; A12539
R;Devinoy, E.; Hubert, C.; Schaerer, E.; Houdebine, L.M.; Kraehenbuhl, J.P.
Nucleic Acids Res. 16, 8180, 1988
A;Title: Sequence of the rabbit whey acidic protein cDNA.
A;Reference number: S01286; MUID:88335562; PMID:3419910
                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000
C;Accession: A93423; B23879; A01227; A92296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 30/1; 75/1; 130/1
C; Superfamily: antileukoproteinase; antileukoproteinase repeat homology
C; Keywords: duplication; milk; proteinase inhibitor
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: whey acidic protein #status predicted <MAT>
F;30-73/Domain: antileukoproteinase repeat homology <ALP1>
F;79-128/Domain: antileukoproteinase repeat homology <ALP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X07943; NID: g1779; PIDN: CAA30764.1; PID: g1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KGPVS---TKPGSCPIILIRCAMLNPP----NRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.3%; Score 79.5; DB 1; Length 134; 34.5%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
15;
                                                                                                                                          81 INSKSGSCPRPLGISVFQDNTIGCWMDSNCPGIQKCC 117
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                     9 VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    whey acidic protein precursor - rabbit
                                                                                                                                                                                                                                                                                                                                    whey acidic protein precursor - mouse C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Conservative
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Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-127 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B23879
   15;
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   Matches
                                                                                                                                                                                                                                                              RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - sea urchin (Strongylocentrotus purpuratus) (fragment)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30272
R;Wessel, G.M.
B;Wessel, G.M.
A;Title: A protein of the sea urchin cortical granules is targeted to the fertilization
A;Reference number: Z20801; MUID:95154582; PMID:7851660
                   Int. J. Androl. 17, 314-323, 1994
A/Title: Gene expression in the dog epididymis: a model for human epididymal function.
A/Reference number: 154768; MUID:95263175; PMID:7744511
A/Accession: 154768
A/Rolecule type: mRNA
A/Rolecule type: mRNA
A/Residues: 1-124 <ELL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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A;Experimental source: strain Bristol N2; clone R12A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein R12A1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1.1142 <WES>
A;Cross-references: EMBL:U1/377; NID:g596089; PID:g596090; PIDN:AAA85106.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----POSNTAYGGNNDPGVCVDNCFQDTDCPEPMKCCAAPSECGLTC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NRCLKDTDCPGIKKCC--EGSCGMAC 53
                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S77395; NID:9945180; PIDN:AAB34264.1; PID:9945181
C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;76-123/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 85; DB 2; Length 1142; ilarity 30.3%; Pred. No. 0.28; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.9%; Score 88; DB 2; Length 124; Best Local Similarity 38.3%; Pred. No. 0.026; Matches 18; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 KEGSCPQVNTDFPQLGLCQDQCQVDSHCPGLLKCCYNGCGKVSCVTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Pauley, A.; Andrews, S. submitted to the EMBL Data Library, July 1997 A; Description: The sequence of C. elegans cosmid R12Al. A; Reference number: Z21118 A; Reference: T32060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: T30272
A,Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.29;
   R;Ellerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%;
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ses 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 75/1; 139/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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Best_Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                    B84868
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R;Kato, I.; Tominaga, N.
FRATO, I.; Tominaga, N.
Fred. Proc. 38, 9822, 1979
A;Title: Trypsin--subtilisin inhibitor from red sea turtle eggwhite consists of two tand A;Reference number: A01224
A;Reference number: A01224
A;Recession: A01224
A;Recession: A01224
A;Residues: 1-110 cKAT>
C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain A;Residues: 1-10 cKAT>
C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain C;Comment: This inhibitor antileukoproteinase inhibitor homology cBD:>
F;8-58/Domain: antileukoproteinase repeat homology cALP>
F;8-58/Domain: antileukoproteinase repeat homology cALP>
F;1/Modified site: pyrrolidone carboxylic acid (GIN) #status experimental
F;8-58,17-41,33-54,67-93,76-97,80-92,86-101/Disnified bonds: #status predicted
F;18/Inhibitory site: Lys (trypsin) #status predicted
Nucleic Acids Res. 18, 3641, 1990

A;Title: Complete sequence of the rabbit whey acidic protein gene.

A;Reference number: S12586; MUID:90301490; PMID:2362817

A;Accession: S12586

A;Molecule type: DNA

A;Residues: 1-127 < THE>

A;Cross-references: EMBL:X52564; NID:g1783; PIDN:CAA36798.1; PID:g1784

B;Cordon. S.M.; Kindt, T. J.

B;Cochem. Biophys Res. Commun. 72, 984-990, 1976

A;Title: BIP: A low molecular weight protein coisolated with beta-2 microglobulin.

A;Residues: 27-38, 27, 40-47, 87, 49-51 <GOR>
C;Genetics:

A;Introns: 28/1; 70/1; 123/1

C;Superfamily: antilenter
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C;Species: Caretta caretta (loggerhead)
C;Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable endochitinase (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 SAAGGSCRTPIIVPTPKAGRCPWVQAPMLSQLCEELSDCANDIECRGDKKCCFSRCAMRY 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology C;Keywords: phosphoprotein F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.8%; Score 74.5; DB 1; Length 110; 34.8%; Pred. No. 0.58; ive 4; Mismatches 15; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.9%; Score 78; DB 2; Length 127; Best Local Similarity 33.3%; Pred. No. 0.28; Matches 21; Conservative 4; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;20-127/Product: whey acidic protein #status predicted <MAT> F;28-68/Domain: antileukoproteinase repeat homology <ALP1> F;74-121/Domain: antileukoproteinase repeat homology <ALP2>
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Best Local Similarity 34.89
Matches 16; Conservative
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Nap position: 2
C,Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-333 *LED>
A;Residues: 1-333 *LED>
A;Cross-references: EMBL:AF016679; PIDN:AAB66161.1; GSPDB:GN00023; CESP:T28C12.6
A;Experimental source: strain Bristol N2; clone T28C12
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A;Cross-references: EMBL:AF039051; PIDN:AAB94263.1; GSPDB:GN00023; CESP:C14C6.5
A;Experimental source: strain Bristol N2; clone C14C6
                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: AE002093; NID: 92281110; PIDN: AAB64046.1; GSPDB: GN00139
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32058
R;Ledwith, J.; Wohldmann, P.; Graves, T.; Bradshaw, H.
A;Describtion: The sequence of C. elegans cosmid T28C12.
A;Reference number: Z21117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
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C;Superfamily: Caenorhabditis elegans hypothetical protein F48G7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.7%; Score 71; DB 2; Length 273; 40.6%; Pred. No. 2.7; ive 4; Mismatches 5; Indels
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R;David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C14C6.
A;Reference number: Z21210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T28C12.6 - Caenorhabditis elegans
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Best Local Similarity 40.6'
Matches 13; Conservative
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C;Species: Schistosoma mansoni
C;Date: 22-Apr-1993 #sequence_revision 19-May-1994 #text_change 18-Jun-1999
C;Accession: B45558; S27837
C;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of epi
A;Reference number: A45558; MUID:92365727; PMID:1501637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 752-1407, 'R', 1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
                                                                                                                                                               C;Species: Homo sapiens (man)
C;Accession: A54105, 817063; 531101
C;Accession: A54105, 817063; 531101
R;Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguineti, C.; Bonadio, J.; Mecham, F. A.; Call Baiol. 124, 855-863, 1994
A;Title: Structure and expression of fibrillin-2, a novel microfibrillar component preferance number: A54105; MUID:94165150; PMID:8120105
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2918 <ZHA>
A;Cross-references: GB:U03272
A;Cross-references: GB:U03272
B;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P. Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two ffere A;Reference number: S17062; MUID:91304567; PMID:1852206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermal growth factor receptor homolog precursor (splice form 2) - fluke (Schistosoma
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A;Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928 <LEE>
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R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.
submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 2918;
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Pred. No. 53;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, December 1992
A;Reference number: S31101
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C,Superfamily: fibrillin 1; EGF homology
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                                                                                                                                      ibrillin-2 precursor - human
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nes 22; Conserva
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A; Residues: 1-333 <SHO1>
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A;Status: preliminary
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
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A, Residues: 1-1360 <COU>
A, Cross-references: EMBL.API25461; PIDN:AADI2852.1; GSPDB:GN00020; CESP:Y8A9A.2
A, Experimental source: strain Bristol N2; clone Y8A9A
C, Genetics:
C, Genetics: A, RA9A.2
A, Map position: 2
A, Map position: 2
A, Map position: 2
A, Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 718/3; 848/2; 944/2; 1044/2;
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C;Genetics:
A;Gene: WTH1801
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y8A9A.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                      214 QGSCCTNPSQASCPSVTSMNINCRKLRSVNWCNNDFDCRGGSTTASMCCPTGC 266
                                                                                                                                                                                                                                                                                                             6 KGPVSTKP--GSCPIIL---IRCAMLNPPNRCLKDTDCPG----IKKCCEGSC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TKPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEG-----SCGM-ACFVP 56
                                                                                                                                                               20.6%; Score 67.5; DB 2; Length 333; 34.0%; Pred. No. 7.2; tive 2; Mismatches 24; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%; Score 67; DB 2; Length 1360; 28.3%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                 A;Map position: 5
A;Introns: 53/2; 89/3; 117/1; 157/2; 181/1; 244/2; 286/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T33922
R;Courtney, L.; Langston, Y.; Drone, K.; Mead, K.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid Y8A9A.
A;Reference number: Z21439
A;Accession: T33922
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 34.0%
Matches 18; Conservative
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Matches 21; Conserv
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                                    A; Gene: CESP: T28C12.6
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C;Genetics:
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1 Similarity 31.4%;
16; Conservative
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A; Residues: 1-493 <PEC>
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                 A;Status: preliminary
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Cyhocemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Blochem. Parasitol: 53, 17-32, 1992
AyTitle: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep AyEcterace number: A4558; MuID:92365727; PMID:1501637
AyAccession: C4558
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A; Description: Alternative splicing of the Schistosoma mansoni gene encoding a homologue
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C; Species: Schistosoma mansoni
C; Date: 22-Apr-1993 #sequence_revision 19-May-1994 #text_change 18-Jun-1999
C; Accession: D45559; S27839
R; Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
A; Elochem. Parasitol. 53, 17-32, 1992
A; Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep A; Reference number: A45558; MUID:92365727; PMID:1501637
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 -RAC 273
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D45558
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Balbiani ring 3 protein - midge (Chironomus tentans)
(Species: Chironomus tentans
(Species: Chironomus tentans
(Spaces: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
(SAccession: 808167
R:Paulsson, G.; Lendahl, U.; Galli, J.; Bricsson, C.; Wieslander, L.
A:Paulsson, G.; Landahl, B.; Bricsson, C.; Wieslander, L.
A:Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structy
A:Reference number: 808167; WUID:90172404; PMID:1689777
                                                                                                                                                                                                                               C.Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology C;Keywords: alternative splicing; ATP; receptor F;1-19/Domain: signal sequence #status predicted <SIG>F;20-366/Product: epidermal growth factor receptor homolog 5 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T01206
R;Pechan, T.; Jiang, B.; Ye, L.; Steckler, D.; Luthe, D.S.; Williams, W.P.
submitted to the EMBL Data Library, August 1997
A;Description: cDNA clones encoding cysteine proteinases from corn (Zea mays L) Callus.
A;Reference number: Z14270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:AF019146; NID:g2425063; PIDN:AAB88262.1; PID:g2425064
A,Experimental source: strain Mp708; callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Zea mays (maize)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
A;Molecule_type: DNA^*
A;Residues: 1-366 < SHO>
A;Cross-references: EMBL:M86399; NID:g160963; PIDN:AAA29869.1; PID:g160964
A;Note: sequence extracted from NCBI backbone (NCBIP:111133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 GSCPVVNGRGYCWGPKPEMCQKMLKCAN-NPDNYCLGGRATTQPCLEECLGGCETRPGNC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LIRCAMLNPPNRCL--KDTDCPGIKKC---CE---GSC 49
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A;Residues: 1-1700 cPAU>
A;Cross-references: GB:X52263; NID:g7057; PIDN:CAA36506.1; PID:g7058 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCC-----EGSC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 65; DB 2; Length 493; 31.4%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
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C;Keywords: cysteine proteinase; hydrolase
F;188,324,344/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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A, Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 65;
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RESULT 45 A45558

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A;Cross-references: EMBL:Z82265; NID:e1297698; PIDN:CAB05175.1; GSPDB:GN00022; CESP:F02H6
A;Experimental source: clone F02H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-293 <WIL>
A;Residues: 1-293 <WIL>
A;Cross-references: EMBL:Z82265; NID:e1297698; PIDN:CAB05174.1; GSPDB:GN00022; CESP:F02H6
A;Experimental source: clone F02H6
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T16859
R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Reference number: 218591
A;Reference number: 218591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F02H6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;bacies: Caenorhabditis elegans
C;baces: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20524
R;McMurray, A.
                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKC-CEGS-----CG-MACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKC-CEGS-----CG-MACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 TSNGVCATTCGACSNLNYTRICLSD----GLKNCPCVGSTTITQPCGTQACNYPR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64, DB 2, Length 293;
Pred. No. 15;
3; Mismatches 20; Indels
85 GSSCCKPVCCCVPVCSCSSCGGCKPCCQSSC--CKPCCSSGCGSSC 129
                                                                                                                                                                                                                       hypothetical protein F02H6.6 - Caenorhabditis elegans
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17;
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A;Reference number: 219286
A;Accession: T20524
                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1996 A;Reference number: Z19286 A;Accession: T20523
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A; Introns: 26/1; 104/2; 178/3; 204/1
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Matches 20; Conservative
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Best Local Similarity 36.4%
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              R; McMurray, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N; Contains: protein-tyrosine kinase (BC 2.7.1.112)
C; Species: Schistosoma mansoni
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A45558; S27836
R; Shoemaker, C B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A; Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep. A; Reference number: A45558; MUD: 92365727; PMID:1501637
A; Reference number: A45558; MUD: 92365727; PMID:1501637
A; Residues: 1-177 (2400)
A; Reference sidues: 1-177 (2400)
A; Residues: 1-177 (2400)
A; Residues: 1-177 (240)
A; Residues: 1-177 (240)
A; Residues: 1-177 (240)
A; Residues: Lill Allowed Franct from NCBI backbone (NCBIP:111129)
C; Genetics:
A; Genetics:
A; Genetics:
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R,Wood, L., Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Telle: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; WUID:91065960; PMID:2250030
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C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 GSCPVVNGRGYCWGPKPEMCQKMLKCAN-NPDNYCLGGRATTQPCLEECLGGCETRPGNC 270
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                                                                                                                                                                                                Gaps
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A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                    267 PNTCE---CGCAQLINCPDNKKANKETCQCECKEVKKCNGGQVFCKDSCSCVC 315
                                                                                                                                                                                                                                                                      13 PGSCPIILIRCAMLNPPN--RCLKDT---DCPGIKKC-----CEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1717;
                                                                                                               Length 1700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                            14; Indels
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                                                                                                               Query Match 19.9%; Score 65; DB 2; Best Local Similarity 32.7%; Pred. No. 45; Matches 17; Conservative 7; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
19.9%; Score 65; DB 1
Best Local Similarity 31.2%; Pred. No. 45;
Matches 20; Conservative 10; Mismatches
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                                                  C; Superfamily: unassigned Balbiani ring proteins
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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C;Species: Mus musculus "nouse mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002
C;Accession: R;A;Nemirez, F.
J;Cell Biol. 129, 1165-1176, 1995
J;Cell Biol. 129, 1165-1176, 1995
J;Cell Biol. 129, 1165-1176, 1995
J;Cell Biol. 129, 1165-1176, 1995
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Mucleic Acids Res. 18, 5577, 1990
A;Title: Nucleotide and deduced amino acid sequence of the bovine adenovirus type 7 prot. A;Reference number: S11434; MUID:91016864; PMID:2216744
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2012 ECVALPGSCSPGTCQNLEGSFRC--ICPPGYEVRSENCIDINECDEDPNICLFGSCTNTP 2069
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                                                                                                                                               571 QEPIKLPVCSNGMISQKRCLVAAECGLNLECSNGGCCPIPF--C----PNGVTARGRCS 623
                                                       33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1.2907 <ZHA>
A;Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
                                                       --STKPGSCPIILIRCAMLNPPN-----RCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.3%; Score 63; DB 2; Length 2907;
Best Local Similarity 30.9%; Pred. No. 1.1e+02;
Matches 21; Conservative 7; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
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C;Species: Mastadenovirus bos7 (bovine adenovirus 7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: fibrillin 1; EGF homology F;1239-1274/Domain: EGF homology <EGF1>F;2488-2523/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                          624 OVNGCPMGOACMEGIC---CPLPK 644
                                                                                                                                                                                                                                  34 KDIDCPGIKKCCEGSCGMACFVPQ
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A,Molecule type: nucleic acid
A,Residues: 1-202 <CAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrillin-2 precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                       2 QEPVKGPV-
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C. Accession: T16840
R. Gate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
R. Gate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
R. Gate: 20-Sep-1999 #sequence_revision 20-Sep-1999
R. Gate: 1. T16840
A. Description: The sequence of C. elegans cosmid T10E10.
A. Reference number: 218588
A. Accession: T16840
A. Accession: T16840
A. Accession: T16840
A. Residues: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-1101 GEI>
A. Residues: 1-1101 GEI>
A. Residues: 1-1101 GEI>
A. Residues: Sequence: EMBL: U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E1
C. Genetics:
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1296 < DUZ>
A;Residues: 1-1296 < DUZ>
C,Genetics: EMBL:U40030; NID:g1055164; PID:g1055165; PIDN:AAA81133.1; CESP:T13CZ
C,Genetics: A;Gene: CESP:T13C2.5
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C;Species: Gallus gallus (chicken)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Date: 28-Sep-1990
R;Doral, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A;Title: An alternative non-tyrosine protein kinase product of the c-src gene in chicken A;Reference number: A35650; MUID:90318371; PMID:2115117
A;Accession: A35650
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                       A;Introns: 62/3; 93/3; 124/3; 142/1; 212/1; 293/1; 336/2; 406/3; 437/1; 508/1; 584/1; 6d
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A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GSCPIILIRCAMLNPPNRC-----GSCG 50
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A,Residues: 1-219 <DOR>
A,Cross-references: GB:M57290; NID:g212703; PIDN:AAA49076.1; PID:g212704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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Local Similarity 22.7%; Pred. No. 14;
les 17; Conservative 9; Mismatches 24: Indele 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 19.3%; Score 63; DB 2; Length 1101; Best Local Similarity 27.4%; Pred. No. 52; Matches 23; Conservative 6; Mismatches 17; Indels 3
                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T10E10.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PVKGPVSTKPGSCPI ---ILIRC--AMLNPPNRC---
                                                                                                                                                                                                                                                                                                                                                               Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                               19.68;
                                                                                                                                                                                                                                                                                                                                                                                                    28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 IGVCATFDSCKKPQ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 -GIKKCCEGSCGMAC 53
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Sur protein - chicken
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Matches
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19.0%;
                                                        Conservative
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                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: GDB:TFF2; SML1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 GSCGMACF 54
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A; Status: preliminary
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                                                        16;
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: 34.577 Througher Levision 4/-Jan-1995 R;Accession: 34.577 C;Accession: 4.5.777 Through 2.7. Bur. J. Biochem. 218, 183-194, 1993 Bur. J. Biochem. 218, 183-194, 1993 Bur. J. Biochem. 218, 183-194, 1993 Bur. J. Biochem. 218, 183-194, 1993 Bur. J. Biochem. 218, 183-194, 1993 Bur. J. Biochem. 218, 183-194, 1993 Bur. Bur. J. Hunziker, P.E.; Kaegi, J.H.R.; F. Bur. J. Biochem. 218, 183-194, 1993 Bur. Barica and four monomeric forms of metal A;Reference number: S39416; MUID:94062828; PMID:8243463
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: 833422
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F. R. Biochem. 218, 183-194, 1993
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal A;Reference number: 839416; MUID:94062828; PMID:8243463
                                                                                                                                                                                                                                                                                                                                                                           67
                          RiRowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
                                                                                                                                                                                                                                                                                                         A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1;
1679/3; 1729/1; 1761/3: and colling more homeload
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metallothionein 20-IIIb - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 SPKPGSPPL----CACLSGFGGPDCLTPPAPPGCGPPSPCLHNGTCTETPGL----GNP 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STKPGSCPIILIRCAMLN--------PPNRCLKD---TDCPGIKKCCEGSC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                      A,Accession: T09059
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-1964 < ROW>
A,Residues: 1-1964 < ROW>
A,Cross-references: EMBL.AF030001; NID:92564945; PID:92564947
                                                                                                                                                                                                                                                                                                                                                                                                                        C.Superfamily: unassigned EGF-related proteins; EGF homology C;Keywords: receptor; signal transduction F;514-545/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PGPCNCI-----ETNVCICGTGCSG--KCCQ--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.1%; Score 62.5; DB Best Local Similarity 29.9%; Pred. No. 91; Matches 20; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 62; 39.0%; Pred. No.
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A;Residues: 1-71 < MAC>
C;Superfamily: metallothinnein
C;Keywords: chelation; metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: chelation; metal binding
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Best Local Similarity 39.08
Marches 16; Conservative
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A, Residues: 1-71 <MAC>
C, Superfamily: metallothionein
                                                                                                              A; Reference number: Z16543
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C; Accession: T09059
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R.Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
A.Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-rid
A.Reference number: S60314; MUID:94149288; PMID:7508963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pS2 in
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: 21.NOv-1993 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
C;Accession: S01-293
R;Tomasetto, C.; Rio, M.C.; Gautier, C.; Wolf, C.; Hareuveni, M.; Chambon, P.; Lathe, EMBO J. 9, 407-414, 1990
A;Title: hSP, the domain-duplicated homolog of pS2 protein, is co-expressed with pS2 in A;Reference number: S12371; MUID:90151615; PMID:2303034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;32-73/Domain: trefoil homology <TRF1>
F;82-122/Domain: trefoil homology <TRF2>
F;30-128,32-59,43-58,53-70,82-108,92-107,102-119/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Date: 12-Apr_1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X73462; NID:g512030; PIDN:CAA51841.1; PID:g512031
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ARRPAPGSAPRPGAMCLAGSEKPSPC----OCSRLSPHNR----TNCGFPGITSDQCFD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;MOlecule type: mRNA
A;Residues: 1-130 <TOM>
A;Cross-references: EMBL:X51698; NID:g36558; PIDN:CAA35995.1; PID:g36559
                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: spasmolytic protein; trefoil homology
C;Keywords: duplication; hormone; pancreas
F;1-24/Domain: signal sequence (fragment) #status predicted <SIG>F;25-130/Product: spasmolytic protein #status predicted <MAT>
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DB 2; Length 71;
                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                 13 PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                1 PGPCNCI-----ETNVCICGTGCSG--KCCO--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                        spasmolytic protein 1 precursor - human (fragment)
N,Alternate names: trefoil factor 2
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                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%; Score 62; DB 30.9%; Pred. No. 13;
Score 62;
Pred. No. 8
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: GDB:128989; OMIM:182590 A, Map position: 21q22.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hair keratin cysteine rich protein - sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%;
28.6%;
                                  39.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 28.6
Matches 14; Conservative
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4

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A; Cross-references: FlyBase: FBgn0001978
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A;Accession: 840993
A;Wolecule type: DNA
A;Residues: 1-435 <AIN>
A;Crosa-references: EMBL:227078
C;Genetics:
A;Introns: 90/1; 305/3; 379/1; 425/1
                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 27.4% Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 NPRLCTECEGOCPKSC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 ----CEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 829 OPNFSCGMACGKP 841
                                                                 A;Reference number: Z22805
A;Accession: T44598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ----SCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       A; Note: BcDNA.LD22726
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S40993
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Cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis)
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Stacession: S50062; S57920; S46931
B;Kroeger, N.; Bergsdorf, C.; Sumper, M.
B;Kroeger, N.; Bergsdorf, C.; Sumper, M.
B;Kroeger, N.; Bergsdorf, C.; Sumper, M.
B;Ricolar A; Af64683, 1994
A;Title: A new calcium binding glycoprotein family constitutes a major diatom cell wall A;Residues: 1-442 ckRo>
A;Molecule type: mRNA
A;Residues: 1-442 ckRo>
A;Cross-references: EMBL:X80394; NID:9515362; PIDN:CAA56603.1; PID:9515363
A;Molecule type: protein
A;Residues: 30-37 ckRo>
C;Keywords: calcium binding; glycoprotein
B;1-17/Domain: signal sequence #status predicted ckRo>
F;18-29/Domain: signal sequence #status predicted ckRo>
F;18-29/Domain: propeptide #status predicted ckRo>
F;30-442/Product: cell wall glycoprotein, 75K #status experimental ckMI>
                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z19279
A;Accession: T20466
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 < WIL>
A;Residues: 1-178 < WIL>
A;Cross-references: EMBL: Z81493; NID:e1321999; PIDN: CAB04039.1; GSPDB:GN0020; CESP:F01D
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T44598

hypotherical protein [imported] - fruit fly (Drosophila melanogaster)

hypotherizen names: BcDNA.LD2276

C.Species: Drosophila melanogaster

C.Species: Drosophila melanogaster

C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000

C.Accession: T44598

R.Rubin, G.M.; Wan, K.H.; Harvey, D.; Lewis, S.E.; Brokstein, P.; Tsang, G.; Agbayani, A.

n, D.E.; Frise, E.; Galle, R.; George, R.A.; Harris, N.L.; Hoskins, R.A.; Evans-Holm, M.
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                                                                                                                                                                                             hypothetical protein F01D5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.0%; Score 62; DB 2; Length 178; Best Local Similarity 30.2%; Pred. No. 17; Matches 16; Conservative 3; Mismatches 20; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 ŚCPVTCKLCPPTEAPTTLAPCFDDKDTDCASFKQFCSNSKYIPMLKSFCPVTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 PAPAPTPTPPGKLPLMITQSF---PLGRCQGDCD-----RDGDCQSGLKCF 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SCPIILIRCAMLNPPNR---CL--KDTDCPGIKKCCEGS------CGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC--GMACF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.0%; Score 62; DB 2; Length 442; Best Local Similarity 30.2%; Pred. No. 33; Matches 16; Conservative 6; Mismatches 19; Indels
52 PICCQP-TCP-----RPTCCISSCYRP---SCCRSSCGSSCYRP 86
                                                                                                                                                                                                                            C'Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T20466
R;Lloyd, C.
Submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: CESP: F01D5.1
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A; Introns: 124/2
                                                                                                                           RESULT 59
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Cjate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000 CjAccession: T43220 #sequence_revision 11-Jan-2000 #text_change 11-May-2000 CjAccession: T43220 #sequence_revision 11-Jan-2000 #text_change 11-May-2000 K;Pashmforoush, M.; Chan, S.J.; Steiner, D.F. Mol. Endocrinol. 10, 857-866, 1996 A;Title: Structure and expression of the insulin-like peptide receptor from amphioxus. A;Reference number: Z22346; MUID:96408719; PMID:8813726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1363 <PAS>
A;Cross-references: EMBL:S33394; NID:g1911771; PID:g1911772; PIDN:AAB50848.1
C;Superfamily: insulin receptor; protein kinase homology
C;Keywords: hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein KO4H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 02-Aug-1994
C;Accession: S40993
R;Ainscough, R.
submitted to the EMBL Data Library, October 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              772 PCGTKK---PICKLPCSRIHPCDHPPQHNCHSGPTCPPCMIFTTKLCHGNHELRKTIPCS 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 GEC---LIQC----PPDTYQYKDRRCITEEECPNTTNSVWKLHHRKCIPECPSGYTTDIN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.8%; Score 61.5; DB 2; Length 1363; 23.7%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.8%; Score 61.5; DB 2; Length 1106; 27.4%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GSCPIILIRCAMLNPPN-----RCLKDTDCPGI------KKC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 PVSTKPGSCPIILIRCAMLN----PPNRCLKDTDCPG----IKKCCEG-
; Snir, E.; Svirskas, R.R.; Weinburg, T.; Celniker, S.E. submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin-like growth factor-1 receptor - common lancelet N,Alternate names: insulin-like peptide receptor C;Species: Branchiostoma lanceolatum (common lancelet)
                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1106 <RUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AF145679; PIDN: AAD38654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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18;
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                        59
21 PAFNPMRNKIGECTQSHTMCLRAVLLTPHNKKKHTSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPRIL-----KQCKRDSDCPGECICMAHGFCG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 CPIILIRCAMENPPNRCLKDTDCPGIKKC-CEGSCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.5%; Score 60.5; DE
Best Local Similarity 27.3%; Pred. No. 93;
Matches 21; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: seed
C, Superfamily: squash trypsin inhibitor ITD I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: RING finger homology F;193-252/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 CKKRCHSGLCG-ACFEP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 -- KKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                     A;Reference number: Z21973
A;Accession: T41146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein A;Residues: 1-30 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 PVSTKPGSCP----
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ses 14; Conserv
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                                                                                                                                                                                        C; Accession: T41146
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
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                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 68
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                                                                                                                                                                                                                                                                                           A; Variety: strain 229
Cjate: 2:-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T44447; T44244
R;Dominguez, G:; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
A; Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human A;Reference number: 222734; MUID:99412318; PMID:10482553
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                                                                                                                                                                                                                                  Env transmembrane protein gp43 - human immunodeficiency virus type 2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                              Gaps
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  18.7%; Score 61; DB 2; Length 435; 47.6%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 855,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.7%; Score 61; DB 2; Length 855
Best Local Similarity 38.2%; Pred. No. 69;
Matches 13; Conservative 8; Mismatches 11; Indels
                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Residues: 1-855 <BAR>
A,Experimental Source: UC1
A,FXPerimental Source: UC1
C,Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3 protein [imported] - human herpesvirus 6 (strain 229)
C;Species: human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-59 < DONA A;Cross-references: EMBL:AF157706; PIDN:AAD49619.1 A;Experimental source: strain Z29; variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-59 <DO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF157706; PIDN:AAD49687.1 A;Experimental source: strain Z29; variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.5; [
Pred. No. 10;
                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 STKPGSCPIILIRCA -- MLNPPNRCLKDTDCPGI 41
                                                                                                               106 CTSDEDCPTTFKCYQGCCKLA 126
                                                                                     32 CLKDTDCPGIKKCCEGSCGMA 52
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33.3%;
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Best Local Similarity 33.33,
                                           10; Conservative
                        Best Local Similarity
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    Query Match
                                           Matches
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T44147
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A45713
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4 PVKGPVSTKPGSCP---IILIRCAMLNPPNRCLKDTDCP 39

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metallothionein 20-Ib - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 2-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C;Accession: 847576
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Fc
Eur. J. Blochem. 218, 183-194, 1993
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A,Accession: JX0057
probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1077 <HILD.
A;Coss-references: EMBL;AL031907; PIDN:CAA21417.1; GSPDB:GN00068; SPDB:SPCC18.03
A;Experimental source: strain 972h-; cosmid c18
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                                          C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
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C.Species: Momordica charantia (balsam pear bitter gourd)
C.Species: Momordica charantia (balsam pear bitter gourd)
C.Species: 30-7un-1992 #sequence_revision 30-7un-1992 #text_change 23-Mar-1995
C.Accession: JX0657
R.Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 PLLCHPGPCPPCTATVEKFCLCGKESIHARCSNISKVNTEPFRC--ENVCDELLPCGEHT 352
                                                                                                                                                           R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A; Molecule type: mRNA
A; Residues: 1-5376 <GAO>
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    C; Accession: T42629
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C;Species: Mytilus edulis (blue mussel)
C;Species: Mytilus edulis (blue mussel)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: 839420
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F. Eur. J. Biochem. 218, 183-194, 1993
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal A;Reference number: 839416; MUID:94062828; PMID:8243463
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A, Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
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C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                            18.3%; Score 60; DB 2; Length 71; 39.0%; Pred. No. 13; tive 1; Mismatches 12; Indels
                               A,Reference number: S39416; MUID:94062828; PMID:8243463
A,Accession: S47576
A,Molecule type: protein
A;Residues: 1-71 cMAC:
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PGPCNCI-----ETNVCICGTGCSG--KCCR--CGDAC 29
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A,Molecule type: protein
A,Residues: 1-71 «MAC>
C,Superfamily: metallothionein
C,Keywords: chelation; metal binding
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C;Superfamily: metallothionein
C;Keywords: chelation; metal binding
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Best Local Similarity 39.0%;
Matches 16; Conservative
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Matches 16; Conservative
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A;Gene: TN-X
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix; glycoprotein; heptad repeat
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R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot
A;Reference number: Z22080; MUID:98123114; PMID:9452463
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M
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A,Residues: 1-4135 <ELE>
A,Cross-references: EMBL:Y11915; NID:g2462978; PIDN:CAA72671.1; PID:g2462979
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C.Spacies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 EGAEGPPSSPPSAPGSCP-----DDCNDQGRCVRGRCVCFPGYTGPSCSWPSCPGDCHG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.3%; Score 60; DB 2; Length 5376; 39.0%; Pred. No. 3.6e+02; tive 1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
18.3%; Score 60; DB 2; Length 4135;
Best Local Similarity 26.1%; Pred. No. 2.9e+02;
Matches 18; Conservative 6; Mismatches 17; Indels
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R,Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, J. Biol. Chem. 272, 22866-22874, 1997
A,Title: Characterization of the bovine tenascin-X.
                                                                                                  A,Reference number: 222180; MUID:97426436; PMID:9278449
A,Accession: T42629
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, July 1996
A, Description: The sequence of C. elegans cosmid T27E4.
A, Recession: T2524
A, Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 16; Conservative
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R. Zhandbaeva, B.D.; Gening, L.V.; Gazaryan, K.G.

Mol. 1801. 65, 550-555, 1992

A. Title: Cloning and structural characterization of human hair sulfur-rich keratin genes A. Reference number: 837649

A. Reference number: 837649

A. Accession: 837650

A. Structus: preliminary

A. Molecule type: DNA

A. Residues: 1-17, < ZHU>

A. A. Cross-references: EMBL: X63337; NID: 9311879; PIDN: CAA44937.1; PID: 9311880

C. Superfamily: keratin high-sulfur matrix protein IIIA
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Hieference number: A86141; MuID:21016719; PMID:11130712
A;Accession: D96590
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A;Cross-references: GB:AE005173; NID:99857516; PIDN:AAG00871.1; GSPDB:GN00141
                                                    A,Cross-references: EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T27E4.5
A,Experimental source: strain Bristol N2; clone T27E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T24C10.2 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 QEGSSGAVSTRIRWCRPDCRVEGTCLPPCCVVSC---TPPSCCQLHHAEA----SCCRPS 157
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Best Local Similarity 30.4%; Pred. No. 30;
Matches 21; Conservative 7; Mismatches 20; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       32 CLKDTDC--PGIKKCCEGSCGM-ACFV 55
                                                                                                                                                  A,Gene: CESP:T27E4.5
A,Map position: 5
A;Introns: 40/1; 53/2; 98/1; 118/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 YCGQSCCRP 166
Molecule type: DNA;Residues: 1-131 <BRA>
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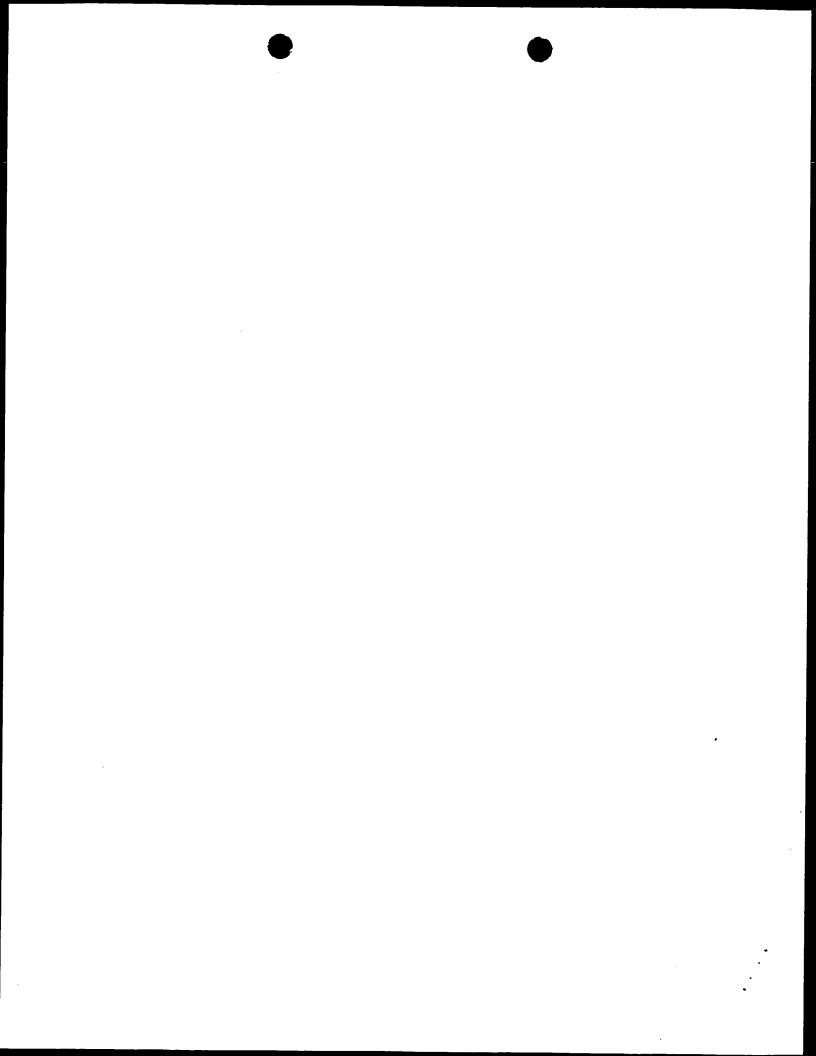
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                                                                                                                                  6 KGPVSTKPGSCPIILIRCAMLNPPN----RCLKD-----TDCPGIKKCCEGSCGMACF
      DB 2; Length 347;
Query Match
Best Local Similarity 30.2%; Pred. No. 50;
Matches 19; Conservative 5; Mismatches 24; Indels
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32, Appl 31, Appl 31, Appl 28, Appl 28, Appl 36, Appl 11,

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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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                     GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-184-964-1
US-08-96-551B-11
US-08-95-97
US-08-97-98-3
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US-08-487-890A-2
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Maximum Match 100%
Listing first 100 summaries
                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents NA:*
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Match
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Perfect score:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Welch, Rod TITLE OF INVENTION: No. 6165723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:
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Best Local Similarity 50.0%; Pred. No. 0.14;
Matches 82; Conservative 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-9166
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-453-702B-166
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                        Valerie
                                                                                                                                                                          US-09-453-702B-166/c

Sequence 166, Application US/09453702B

Parent No. 6365723

GENERAL INFORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                         Perna, N.L.
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Madison
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                                                                                                                                       RESULT 1
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; Sequence 1, Application US/08496944

US-08-496-944-1/c

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Law, Marcus D
APPLICANT: Dietz, John M
TITLE OF INVENTION: Use of Translationally altered RNA to
TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
TITLE OF INVENTION: Monocotyledonous Plant Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "polyprotein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_RNA
LOCATION: 2376-14292
OTHER INFORMATION: /product= "cylindrical inclusion
OTHER INFORMATION: protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "3-prime sequence for HC-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 42937.4451
OTHER INFORMATION: /product= "K2 (6kD protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                            OCTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_RNA
LOCATION: 4452..5744
OTHER INFORMATION: /product= "NIa proteinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5745..7307
OTHER INFORMATION: /product= "NIb replicase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc RNA
LOCATION: 11347.2375
OTHER INFORMATION: /product= "P3 proteinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDMV-B genome"
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIMEr, James Scott
REGISTRATION NUMBER: 36,129
REPRENCE/DOCKET NUMBER: CGC 1
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f: 8543 base pairs
  nucleic acid
)EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_RNA
LOCATION: 7308..8291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8292..8530
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_RNA
LOCATION: 5745..73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_RNA
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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Patent No. 6040496
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Matches
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                                                                                                                                                                                                1679 TCTGARCACGCCATATTGCTGAAATTTTCCACAGTATGACAATTCTGCCCATGATTG 1620
                                                                                                                                                                                                                                                                                 1619 GITTAATTGATCTACGTAACTTTTTTCCATCAGGGTGTATAGGCGCTCGTCATATAGTGC 1560
                                                                                                                                                                                                                                            74 GGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGA 158
                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                      14 TAIGGACGTATACGAGTICTTGGTCAATTICCAGGACACAGATGGTTCGGTCCAAGAACA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 28.8; DB 4; Length 2651; 62.5%; Pred. No. 1.6; cive 0; Mismatches 27; Indels 0
                                                              Query Match 14.1%; Score 29; DB 3; Length 8543; Best Local Similarity 52.0%; Pred. No. 2.2; Matches 65; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
OTHER INFORMATION: /product= "coat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvi--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 216, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.58
Matches 45; Conservative
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MEDIUM TYPE: Diskett
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US-08-961-527-216
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US-08-496-944-1
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62 GGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTTGGATTGGCAACA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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RESULT 4
US-09-184-964-1/C
| Sequence 1, Application US/09184964 |
| Sequence 1, Application US/09184964 |
| Patent No. 6391574 |
| GENERAL INFORMATION: |
| APPLICANT: Rine, Jasper D. |
| APPLICANT: Ashby, Matthew N. |
| TITLE OF INVENTION: PROCESSING ENZYMES |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESS: |
| CORRESPONDENCE ADDRESS: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 TATGAAATCTGACTGGCAGGACTGCATTCAATAAAGAAACGGCCATG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hashimoto, Tamotsu
APPLICANT: Tsujimura, Atsushi
APPLICANT: Tsujimura, Atsushi
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: Process for Preparing Peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
SYSTEM: DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
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                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill road, suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Suyat, Reginald J.
REGISTRATION NUMBER: 28,172
REFERENCE/DOCKET NUMBER: 09272-006004
TELECOMMICATION INFORMATION:
TELEPHONE: 650/322-5070
TELEFAX: 650/854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFIMAKE: FACENCIM KELGESE #1.0, VER CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,964 FILING DATE:
APPLICATION NUMBER: 08/902,774 FILING DATE:
APPLICATION NUMBER: 08/902,774 FILING DATE: 07-AUG-1997 APPLICATION NUMBER: 60/023,491 FILING DATE: 07-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 11, Application US/07696551B
; Patent No. 5232841
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/854-0875
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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STRANDEDNESS: unkno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                              Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                  94025
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-184-964-1
                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
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103 TITGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACT 162
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; Sequence 7, Application US/08552369
; Patent No. 6241989
; GENERAL INFORMATION:
APPLICANT: Scott, Fred W.
APPLICANT: Ngichabe, Christopher K.
TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.1%; Pred. No. 1.9;
Matches 50; Conservative 0; Mismatches 36; Indels 0;
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: NS-DOS/PC-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: UP 2-122166
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-122166
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect
                                         STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lawrence M. Lavin, Jr. REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481-1070
TELECOMMUNICATION: TELECOMMUNICATION: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 TCCAAGGACGCCATACCGAACAAAGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 ACCGATGAAGCCTCCTCTGCCGAAGC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA
                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1796 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: United States
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EDNESS: single
                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                             Dunner
                                                                                                                                     20005-3315
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                             ADDRESSEE:
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                                                                                                                    COUNTRY:
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55 ATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AGGATAACAACATTAAAGGGTTATCGCAGAAGCCAACATGTAGAAATTIGTTGGGGTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 28.2; DB 4; Length 2007; 54.3%; Pred. No. 2.3; tive 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGAC 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Michin, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/487,890A
FILING DATE: 07-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6th Floor, 330 Unviersity Avenue
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/190,789
FILING DATE: 01/27/1994
APPLICATION NUMBER: 07/726,609
FILING DATE: 07/09/1991
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18617.0016
TELECOMMUNICATION INPORMATION:
TELEPHONE: (716) 849-0349
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: capsid protein gene region
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08487890A; Patent No. 5708149
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: feline calicivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                      2007 nucleotides
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Best Local Similarity 54.3%
Matches 57; Conservative
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                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Ontario
TRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim
STREET: 6th Flo
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 0.7-UN-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08478435;
Patent No. 5922323
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Will, Michel
ITILE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCES: 147
CORRESPONDENCE ADDRESS:
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERNE/FOCKET NUMBER: 1038-466 MIS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(121..2100, 2117..4852)
                      APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite 701, 330 University: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Robin
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Wang, Yan-Ping
APPLICANT: Wang, Yan-Ping
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Mixin, Andrew
APPLICANT: Suite 701, 330 Unviersity Avenue
CITY: Toronto
STAFE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:VG
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
join(121..2100, 2117..4852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08337483 Patent No. 5922562
                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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, LOCATION:
US-08-478-435-3
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                                                                                                                                                                                                                                                                                          Query Match
13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/478,377,483
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US/08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US/08/148,968
FILING DATE: 08-NOV-1993
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/148,968
FILING DATE: 08-NOV-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Locsmore, Sheena
APPLICANT: Locsmore, Scheena
APPLICANT: Arkness, Anthony
APPLICANT: Schryvers, Anthony
APPLICANT: Gray-Owen, Scott
APPLICANT: Tang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCEDORGET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                         join(121..2100, 2117..4852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08478373
Patent No. 5922841
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(416) 595-1163
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                      LENGTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-478-373-3
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                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                          13.7%; Score 28.2; DB 2; Length 5009; 64.6%; Pred. No. 3.4; tive 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loosmore, Sheena
APPLICANT: Loosmore, Robin
APPLICANT: Barryers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/474 677 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
TELEPHONE: 416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                     join(121..2100, 2117..4852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995
07-JUN-1995
08-JUN-1995
JN: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/08474671; Patent No. 6008326
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 64.69
Matches 42; Conservative
                                            LENGTH: 5009 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07
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                                                                                                                                                                                                                                                                                                                                                                                                         202 CCTAG 206
                                                                                                                                                 NAME/KEY:
LOCATION:
US-08-478-373-3
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US-08-474-671-3
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                                                                                                                                                                                                                                                                                                     0; Gaps
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Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
ATTANC DATE: OF NOW, 1003
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREFT: Suite 701, 330 Unviersity Avenue CITY Toconto
STATE: Ontario
                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-474-671-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP. MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1038-511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08483577A Patent No. 6015688 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Loosmore, Sheena APPLICANT: Harkness, Robin APPLICANT: Schryvers, Anthony APPLICANT: Chong, Pele APPLICANT: Gray-Owen Scott APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Andrew APPLICANT: Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                    LENCTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5009 base pairs
SEQUENCE CHARACTERISTICS:
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1579 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                             13.7%; Score 28.2; DB 3; Length 5009; 64.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Young, Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Minchin, Andrew
APPLICANT: Minchin, Andrew
APPLICANT: Minchin, Andrew
APPLICANT: Minchin, Andrew
APPLICANT: Minchin, Andrew
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Sim & McBurney
: 6th Floor, 330 University Avenue
Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                             CDS
join(121..2100, 2117..4852)
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PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-UNN-1995
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRICR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08897438 ; Patent No. 6262016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I
REGISTRATION UNUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPOWNUNICATION INFORMATION:
TELEPAN: (416) 595-1155
TELEPAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1639 CATGG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 CCTAG 206
                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-483-577A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-897-438-3
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08637654

patent No. 6358727

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Larkness, Robin E

APPLICANT: Gray-Owen, Scott

APPLICANT: Gray-Owen, Scott

APPLICANT: Amn-Ping

APPLICANT: Murdin, Andrew D

APPLICANT: Harkness And Ping

APPLICANT: Harkness And Ping

APPLICANT: Harkness 147

CORRESPONDENCE SEQUENCES: 147

NUMBER OF SEQUENCES: 147

ANDREGEDER ADDRESS:
                                                                                                                                                                              / Match 13.7%; Score 28.2; DB 4; Length 5009; Local Similarity 64.6%; Pred. No. 3.4; onservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILING DATE: 05-MG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(121..2100, 2117..4852)
                                                                                                     ; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-897-438-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-595
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
LENGTH: 5009 base pairs
                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          · TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                           TOPOLOGY: linear
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STREET: 64...
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; LOCATION:
US-08-637-654-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-637-654-3
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                                                                                   FEATURE:
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                                                                                                        142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                       0; Gaps
Query Match
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UPERALING SISIEM: EL-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,518
FILING DATE: 17-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/337,483
FILING APPLICATION NUMBER: US 08/483,577
FILING APPLICATION NUMBER: US 08/483,577
RAPLICATION NUMBER: US 08/483,577
FILING APPLICATION NUMBER: US 08/483,577
FILING APPLICATION NUMBER: US 08/175,116
FILING APPLICATION NUMBER: US 08/175,116
FILING APPLICATION NUMBER: US 08/175,116
FILING APPLICATION NUMBER: US 08/148,968
FILING APPLICATION NUMBER: US 08/148,968
FILING APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTONEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/148,968
FILING DATE: US NOV-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anchony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6th Floor, 330 Unviersity Avenue CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(121..2100, 2117..4852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08649518; Patent No. 6361779; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24,973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canada
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                                                                                                                                                                                                                                                                             1639 CATGG 1643
                                                                                                                                                                                                                            202 CCTAG 206
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US-08-649-518-3
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LOCATION:

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1627 TICTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
                       142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
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                                                                                                                                                                                                                                                                                                                               APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Michel
TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: O'-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038-462 MIS:vg
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join(169..2148, 2165..4900)
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PELING DATE:

CLASSIFICATION 194

CLASSIFICATION 194

CLASSIFICATION 194

CLASSIFICATION 1975

PRIOR APPLICATION 1978:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1933

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1933

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                Sequence 2, Application US/08478435 Patent No. 5922323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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STREET: Surrary: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                       1687 CATGG 1691
                                                                                                             202 CCTAG 206
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; LOCATION:
US-08-478-435-2
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                                                                                                                                                                                                                      RESULT 17
US-08-478-435-2
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                                                                                                                                                            0; Gaps
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                                     Query Match
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 28.2; DB 1; Length 5033; 64.6%; Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
STATE: Oncario
COUNTRY: Oncario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FLING DATE: 07-JUN-1993
CLASSIFICATION: 435
FRICK APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FRICK APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FRICK APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATPONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 147
CARRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE / DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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6th Floor, 330 Unviersity Avenue
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: LOOSMOYE, Sheena
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LOOSMOTE, Sheena APPLICANT: Harkness, Robin APPLICANT: Schryvers, Anthony APPLICANT: Chong, Pele APPLICANT: Gray-Owen, Scott APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Andrew APPLICANT: Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Conservative
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US-08-487-890A-2
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US-08-487-890A-2
US-08-649-518-3
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Gaps

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142 TCCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGITAITAT 201
                           1627 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
142 TCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                          APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
SAPLICANT: Boltyvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Mardin, Andrew
APPLICANT: Mardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & W.T.
STREFT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08 NOV-1994
CLASSIFTCATHON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038-410 MIS:jb
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LOCATION: join(169..2148, 2165..4900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
                                                                                                                                                                                                                        Sequence 2, Application US/08337483 Patent No. 5922562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
STATE: Ontario
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US-08-478-373-2
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US-08-337-483-2
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1627 İTCITATTAGGİÇAÇCGTAÇICÇÇAAĞGAĞGAĞATAĞÇATAĞĞAAĞTGGAAATAT 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
APPLICATION NUMBER: US 08/148,968
                                                                                         APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Wurdin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McDuriey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038-463 MIS:vg
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                                                                                                                                                                                                                                                                                                                                E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(169..2148, 2165..4900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALK: MAD ALLY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/08478373;
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.65
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 Toronto
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LOCATION:
US-08-478-373-2
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US-08-474-671-2
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GENERAL INFORMATION:
                                           APPLICANT:
APPLICANT:
APPLICANT:
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                                APPLICANT: LOOSMOTE, Sheena
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Barkness, Robin
APPLICANT: Choryers, Anthony
APPLICANT: Chory, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Mirchel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-UNN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
join(169..2148, 2165..4900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08483577A; Patent No. 6015688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                  GENERAL INFORMATION:
APPLICANT: LOOSMON
APPLICANT: HARKNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1687 CATGG 1691
Patent No. 6008326
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LOCATION:
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1627 TTCTTATTAGGTCACCGTACTCCCAAGGACGACATACCTAAAACAGGAAGTGCAAAATAT 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
                                                                                                                                                                         APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
Suite 701, 330 Unviersity Avenue
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US-08-483-577A-2
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US-08-897-438-2
; Sequence 2, Application US/08897438
; Patent No. 6262016
; PAPLICANT: LOOSMOIE, Sheena
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
ITYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                           Harkness, Robin
Schryvers, Anthony
Chong, Pele
Loosmore, Sheena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Ontario
COUNTRY: Canada
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STREET: Sur.
TTW: Toronto
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ZIP: M5G 1R7
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APPLICANT:
APPLICANT:
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APPLICANT:
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Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0;
                APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Wurdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
                                                                                                                                                                                                                6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME_KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
US-08-897-438-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY AGENT: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY AGENT: UN ON-1993
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
Harkness, Robin
                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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STREET: bun
TTY: Toronto
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  APPLICANT:
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Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0;
                                                                                     APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Middin, Andrew D
APPLICANT: Klein, Michel H
APPLICANT: Klein, Michel H
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: join(169.2148, 2165..4900)
US-08-637-654-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-649-518-2
; Sequence 2, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schryvers, Anthony
Chong, Pele
Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
                                          Schryvers, Anthony B
Chong, Pele
Loosmore, Sheena M
                         Harkness, Robin E
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
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Patent No. 6358728
GENERAL INFORMATION:
APPLICANT: Simon, Andras
APPLICANT: Exiksson, Ulf
APPLICANT: Brison, Thaddeus P.
APPLICANT: Berson, Eliot
APPLICANT: Wamanoto, Hioyuji
TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
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TILLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 160
CORRESPENDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
STATE: Oncario
CUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/49,518
FILING DATE: 17-MAY-1996
CLASSIFICATION NUMBER: US 08/43,577
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/43,577
FILING DATE: 08-NOV-1995
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: US 08/175,116
FILING DATE: US 08/175,116
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LOCATION: join(169..2148, 2165..4900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 42; Conservative
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FEATURE:
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US-09-880-427-2/c
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APPLICANT: Simon, Andras
APPLICANT: Eriksson, Ulf
APPLICANT: Eriksson, Ulf
APPLICANT: Brisson, Ulf
APPLICANT: Brisson, Eliot
APPLICANT: Berson, Eliot
APPLICANT: Yamamoto, Hioyuji
TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
FILE REFERENCE: LUD 5601
CURRENT PFLING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 5
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NAME/KEY: unsure
LOANION: 5357, 5448
OTHER INFORMATION: nucleotide not determined
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LOCATION: 5357, 5448
OTHER INFORMATION: nucleotide not determined
US-09-306-538B-2
FILE REFERENCE: LUD 5601
CURRENT APPLICATION NUMBER: US/09/880,427
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/306,538
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09306538B; Patent No. 6372463; GENERAL INFORMATION:
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; Patent No. 6231863
; GENERAL INFORMATION:
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Best Local Similarity 64.6%;
Matches 42; Conservative
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US-09-306-538B-2/c
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US-08-872-056-23/c
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LENGTH: 6330
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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Sequence 1, Application US/09345882
Sequence 1, Application US/09345882
Feature 1. Application US/09345882
GENERAL INFORMATION:
APPLICANT: BOUGUELET, Lydie
APPLICANT: BOUGUELET, Lydie
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REPERENCE: GENEST. 0319
FILE REPERENCE: 1999-06-30
CURRENT FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PATENT UND NOS: 140
                        TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES, MOLECULES, TITLE OF INVENTION: VECTORS AND VACCINES FOR PELINE CALICIVIRUS DISEASE AND TITLE OF INVENTION: METHODS FOR PRODUCING AND USING SAME NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTC 127
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,056
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                                                                                                                                           ADDRESSEE: MCDERMOTT, WILL & EMERY
STREET: 1850 K STREET, N.W., SUITE 500
CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/972,056
PILING DATE: 25-APR-1997
CLASSIFICATION: 24-APR-1997
ATORNET ON 144
ATORNET NUMBER: 37,136
REGISTRATION NUMBER: 37,12-213
TELECOMMUNICATION NUMBER: 37,12-213
TELECOMMUNICATION NUMBER: 37,12-213
TELECOMMUNICATION 1 NPORMATION:
TELEPHONE: (202) 778-8373
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COLAU, DIDIER
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EDNESS: single
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 52; Conserv
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LENGTH: 162450
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    APPLICANT:
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OTHER INFORMATION: 5-128-60 : polymorphic base deletion
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OTHER INFORMATION: 5-143-84 : polymorphic base
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OTHER INFORMATION: 99-1442-224
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INFORMATION: 5-140-120
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OTHER INFORMATION: 5-136-174
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OTHER INFORMATION: 5-133-375
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THER INFORMATION: 5-140-348
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OTHER INFORMATION: 5-135-198
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OTHER INFORMATION: 5-131-395
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OTHER INFORMATION: 5-135-155
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          LOCATION: 72794
OTHER INFORMATION: 5-124-273
                               FEATURE:
NAME/KEY: allele
CATION: 88073
OTHER INPORMATION: 5-127-261
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OTHER INFORMATION: 5-130-257
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NAME/KEY: allele
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FEATURE:
NAME/KEY: allele
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US-09-328-111-653/c
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 72711..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                                       LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
                                                                                                                                                                            or
      or
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1AME/KEZ: allele
JOCATION: 93690..93736
JTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
                                                                                         or
                                                                                       4
OTHER INFORMATION: 5-143-101 : polymorphic base
                                                                                                                                                                          base
                                                                                     base
                                                                                                                                                   LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic
                                                                                     : polymorphic
                                                            LOCATION: 150329
OTHER INFORMATION: 5-145-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 90819..90865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 99094..99140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 88050..88096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93690..93736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 97099..97145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99075..99121
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                                                                                                                           NAME/KEY: allele
                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.6%; Score 28; DB 4; Length 162450; Best Local Similarity 53.7%; Pred. No. 17; Matches 58; Conservative 0; Mismatches 50; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORRATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Derti, Adnan
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE PEPERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1998-06-08
EARLIER PEPLICATION NUMBER: US 60/088,801
EBARLIER PELLONG DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74492 GAGTATCTAATTTTAGTAGGTAGGCAGAAATGTAATTTCTAAAATAG 74539
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 CGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAG 140
INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                              LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
                                                                                                                                                                                                                               LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
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; Patent No. 6262333
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                                                                                                                                                                                                                                                                                  264 roariccarroggcaaacaggaaricargacarragaaaaraggraaagaaaarragcrac 205
                                                                                                                                                                                                                                          34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGGAAC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 2.7;
                                                                                                                                                   Query Match
Best Local Similarity 55.1%; Pred. No. 2;
Matches 54; Conservative 0; Mismatches 44; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mirkov, T. Erik
APPLICANT: Fitzmaurice, Leona Claire
APPLICANT: Fitzmaurice, Leona Claire
ITITE OF INVENTION: Protection of Plants Against Pathogens
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSED: Altch, Even, Tabin & Flannery
STREDT: 135 South LaSalle Street, Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%; Score 2...;
58.5%; Pred. No. 2.7;
58.5%; Indels
...ve 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                   94 GCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGT 131
                                                                                                                                                                                                                                                                                                                                                                               204 CATCTACAGTTTGGTAGCATTGTGACCATAATTAGGGT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MALGELICAL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/798,223A
FILING DATE: 19911125
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,679
FILING DATE: 19-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51984
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 653 LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/07798223A
; Patent No. 5422108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 964 base pairs
NUCLEIC ACID
BDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.5%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 25..459
US-07-798-223A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDALC. 13.
STREET: 13.
CITY: Chicago
CITY: Lilinois
                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                       US-09-328-111-653
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 30
US-07-798-223A-1
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Joseph Control of Application US/08677970

J. Application US/08677970

J. Patent No. 644444

GENERAL INFORMATION:

J. APPLICANT: Michel H.

APPLICANT: Klein, Michel H.

TITLE OF INVENTION: GENES ENCODING MYCOBACTERIAL PROTEINS

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 CGATACAATTTGGGTGGATTGGGAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 cerracialitrereredecirrererererereresendandendendenden 87
358 GCAAAGCATATTGTCAGTGAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27.2; DB 4; Length 4739;
Pred, No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donna T. Ward
APPLICANT: Donna T. Wart
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REPERENCE: RTS-0201
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT PILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%; Scor.
56.8%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-592 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                5: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 ACGACACTTCCAAGGACGCCATACCGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 TCAACATICACACAGGCGCCGTAGCGCA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,970
FILLING DATE: 10-JUL-1996
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10, Application US/09798096; Patent No. 6399378; GENERAL INFORMATION:
                                                    129 TGTGACTAACAGGTCCATAGTT 150
                                                                                            418 CGAGACCATGACGTCAGCAGTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-115
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4739 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.89
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6th F]
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-096-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                              RESULT 31
US-08-677-970-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-677-970-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
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                                                                                                                                                                                                                                                                                                                                                                  Db 10571 AAAAAATTATAGTACATTTATACAACAGAATACTATTCAGCCATAAAAAGAATAAAAT 10512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 10511 CCTGTTÄTTCACAGCAACATGGAACCTGAGGACATTGTGTTTAAGTGGAATAAAGAACAGA 10452
                                                                                                                                                                                                                                                                                                                                                                                                                      127 CCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAA 186
                                                                                                                                                                                                                                                                                                                67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 CGATACAATTTGGGTGGATTGGCAACAACATCCTGTGACTAACAGGTCCATAGTTTTTC 154
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WHITE, Own R.
APPLICANT: WHITE, Own R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%; Score 27.2; DB 4; Length 4403765; Best Local Similarity 56.8%; Pred. No. 58; Matches 50; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                             Length 99500;
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APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jenniel E.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               0; Mismatches 58; Indels
                                                                                                                                                                                                           Score 27.2; DB 4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 196764 réakcarreacacacacacacacacaca 196737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-946-026-13
; Sequence 13, Application US/08946026
; Patent No. 6034218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                             13.2%;
51.7%;
                                                                                                                                                                                                        Query Match
Best Local Similarity 51.73
Matches 62; Conservative
                                                                                                     ORGANISM: Homo sapiens
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 4403765
                     SEQ ID NO 10
LENGTH: 99500
                                                                                                                                                       US-09-798-096-10
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                                                                            TYPE: DNA
                                                                                                                                 FEATURE:
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US-08-961-527-64/c

Sequence 64, Application US/08961527

Patent No. 6420135

Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1221 GGCCTGGTAGTAAACCAGGCCCTGGCTCTTTACCAGCAGTCATCTTCTTGTTGTTGGGG 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAA 71
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1281 CCAGCCAGGAAAAACAAACAACCCGGGGCACATTGGGTAGACT 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 CAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATT 114
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
                      6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/946,026
CLASSIFICATION 1424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/961,527
                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
       ALC.
STREET: bo.
CITY: Seattle
The Washington
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 11873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.7%; Score 26.2; DB 2; Length 116
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels
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TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURTULEN: APPLICATION OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION NUMBER: US/08/970,269A APPLICATION NUMBER: US/08/970,269A FILING DATE: No. 5976803ember 14, 1997 CLASSIFICATION: 435 ATTORNEY/AGRITION: MAME: Adler Ph.D., Benjamin A. REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                 Dr. Benjamin A. Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 32, Application US/09407562
; Patent No. 6294334
                                                                                                                                                                                   Sequence 32, Application US/08970269A
Patent No. 5976803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: D5:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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  138 CAGGTCCATAG 148
                                                        906 GAGGTACCCAG 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
USA
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US-09-407-562-32
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                     US-08-970-269A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION

APPLICANT: DROHAN, William

APPLICANT: DROHAN, William

APPLICANT: HENNIGHAUSEN, Lothar

APPLICANT: HENNIGHAUSEN, Lothar

APPLICANT: HENNIGHAUSEN, Lothar

APPLICANT: HENNIGHAUSEN, Lothar

APPLICANT: HENNIGHAUSEN, Lothar

TITLE OF INVENTION: Expression of a Heterologous Protein C in Mammary Tissue of Tra

TITLE OF INVENTION: Animals Using a Long Whey Acidic Protein Promoter

FILE REFERENCE: 1030623/0150

CURRENT FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-10

PRIOR FILING DATE: 1998-01-01

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-14

PRIOR FILING DATE: 1998-02-14

PRIOR FILING DATE: 1998-02-14

PRIOR FILING DATE: 1998-02-14

PRIOR FILING DATE: 1998-02-14

PRIOR PLING DATE: 1998-02-14

PRIOR PLING DATE: 1998-02-14

PRIOR APPLICATION NUMBER: US 08/198,068

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1499 ACACTITICAAATTCITIGGAAAGATAAGTAATGITTTCITAAAAATGCCAAGGTATATTATGG 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ACAATTIGGGTGGGATTGGCAACAACTICCTGTGACTAACAGGTCCATAGTTTTTCACGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: WAP gene promoter fragment from the C57B/6 mouse strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 12.7%; Score 26.2; DB 4; Length 4122; Local Similarity 60.6%; Pred. No. 16; 28; Indels 0; Pres 43; Conservative 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                        Query Match
12.7%; Score 26.2; DB 4; Length 2723;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 55; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1439 GAATAACTATAAATCTATAGAATCAAAGCGACCAAGTATGAT 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 CACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGTTATTAT 201
REFERENCE/DOCKET NUMBER: PB340P1
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LOCATION: (544)
OTHER INFORMATION: "n" is unknown
MAME/KEY: misc feature
LOCATION: (3377) .. (544)
OTHER INFORMATION: "n" is unknown
                 TELECHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 64: SEQUENCE CHARACTERISTICS: LENGTH: 2723 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09321831
Patent No. 6262336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn version 3.0
                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
US-09-321-831-1/c
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US-08-961-527-64
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RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 26.2; DB 4; Length 11873; 53.4%; Pred. No. 25; tive 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCES: 32
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 10911 ACTITIACCTIGAAGGAACTICITITGAGTAACAIGICACAAG 10953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAG 148
                                                                                                                                                                                                        COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: NO. 6294334ember 14, 1997
CLASSIFICATION:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 11873 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 55, Conservative
NUMBER OF SEQUENCES: 32
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STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                  Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                      STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                              77071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Db 10856 AAGACATACCAGGTCATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAAT 10915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.7%; Score 26.2; DB 2; Length 11878;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 10916 ACTITIACCTIGAAGGAACTICITITGAGTAACATGICACAAG 10958
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,562
COMPUTER: Apple
COMPUTER: Apple
SOPERATING SYSTEM
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/970,269A
FILING DATE: NO. 5976803ember 14, 1997
CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTY: USA
ZIP: 77071
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11878 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: other nucleic acid
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NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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ORIGINAL SOURCE:
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ORIGINAL SOURCE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.7%; Score 26.2; DB 4; Length 11878; Best Local Similarity 53.4%; Pred. No. 25; Matches 55; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08970269A
Patent No. 5976803
Patent No. 5976803
PAPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TIRE.
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: No. 5976803ember 14, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                              other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: other nucleic acid
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NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
REFERENCE/DOCKET NUMBER: D5860
                                                                                                                                                   nucleic acid
EDNESS: double stranded
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EDNESS: double stranded
                TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                LENGTH: 11878 bp
                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 11883 bp
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                                                                                                                                                                                                                                                               HYPOTHETICAL: no
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COUNTRY: USA
ZIP: 77071
                                                                                                                                                                                                                                                                                        ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-970-269A-28
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Db 10861 AAGACATACCAGGTCATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAAT 10920
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                                                                                                                                                                                                                                                                                                     46 AGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTT 105
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                                                                                           12.7%; Score 26.2; DB 2; Length 11883; 53.4%; Pred. No. 25; tive 0; Mismatches 48; Indels 0;
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12.7%; Score 26.2; DB 4; Length 11883;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 12
CORRESPONDEMES ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 10921 ACTITIACCTIGAAGGAACTICTITIGAGIAACAIGICACAAG 10963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334ember 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/407,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Dr. Benjamin A. Adler
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
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ER: D5860
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EDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: DETELECOMMUNICATION INFORMATION: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                  Best Local Similarity
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DESCRIPTION:
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US-08-970-269A-28
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                                                                                                          Query Match
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
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APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
EARLIER APPLICATION NUMBER: 60/154,658
                  EARLIER FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-23
                                                                                                                                                         ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                        47; Conservative
                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (101)..(1366)
US-09-427-501-1
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                      TYPE: DNA
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US-08-951-527-35/c
Sequence 35, Application US/08961527
Patent No. 6420135
Patent No. 6420136
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INFORMINES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-427-501-1/c

| Sequence 1, Application US/09427501
| Sequence 1, Application US/09427501
| Sequence 1, Application US/09427501
| Sequence 1, Application US/09427501
| GENERAL INFORMATION:
| APPLICANT: Connaught Laboratories Limited, Andrew
| TITLE OF INVENTION: CHLAMPIDA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND TITLE OF INVENTION: USES THEREOF;
| FILE REFERENCE: 19724-010
| CURRENT APPLICATION NUMBER: US/09/427,501
| CURRENT FILING DATE: 1999-10-26
| SEALLER PILING DATE: 1999-10-28
| SEALLER FILING DATE: 1999-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4204 AAACAGAAAATACGGGTCAATTTTCTGTTAATATTTTCTAAACCTGGCATTACCAAAGGGC 4145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 19250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                              Db 10921 ACTTTTACCTTGAAGGAACTTCTTTTGAGTAACATGTCACAAG 10963
    106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.7%; Score 26.2; DE
Best Local Similarity 56.3%; Pred. No. 30;
Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4144 AACATTGGCATCATTCTAAGTGGGAAT 4118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 TGGATTGGCAACAACTTCCTGTGACT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 19250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-961-527-35
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1085 AACGTACTGTGGCAGACCAGTCTCCAGCTTTTCTGAGTCCCCCTAAAGTTCCTCCAATAA 1026
                                                                                                                               122 AACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGA 181
12.6%; Score 26; DB 4; Length 1550; 57.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRENT AFFILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER PELING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
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RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
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FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                          1025 ACCAAGCTAGGTTTTCTTTTCC 1004
                                                                                                                                                                                                                                                                      182 ACAAAGCAAGGTGTTATTATCC 203
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R APPLICATION NUMBER: 60/043,314

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569

R APPLICATION NUMBER: 60/043,311

R APPLICATION NUMBER: 60/043,311

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,674

R APPLICATION NUMBER: 60/043,674

R APPLICATION NUMBER: 60/043,674

R APPLICATION NUMBER: 60/043,674

R APPLICATION NUMBER: 60/043,674

R APPLICATION NUMBER: 60/043,413

R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,580
R FILING DATE: 1997-04-11 R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056, 889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 893
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 630
R FILING DATE: 1997-08-22 PILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
FTI-ING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: 60/047,500 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,637 1997-05-23 FILING DATE: 1997-08-22 ILING DATE: 1997-08-22 FILING DATE: 1997-04-1 LING DATE: EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER DE LEA EARLIER EARLIER EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,881 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,874 APPLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/047,589 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/048,964 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 60/047,594 EARLIER APPLICATION NUMBER: 60/056,862 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,887 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,908 EARLIER FILING DATE: 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/( EARLIER FILING DATE: 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-04-FILING DATE: FILING DATE: FILING DATE: EARLIER PEARLIER PEARLIER EARLIER FEARLIER FEARLIER EARLIER / EARLIER / EARLIER / EARLIER

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APPLICATION NUMBER: 60/056,888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 ACCCAGAGGAAATCCGAGGGGGAGGCCTGCTTAAGTACTGCAACCTCTTGGTGAGGGGCT 674
                                                                                                                                                                                                                                                                                                                                                      31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGC 90
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 TTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAGGTGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         675 rraggecegecreargargaarcaagaceerreaaaggerarargr 719
                                                                                                                                                                                                                                                                                                       0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
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EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1908-03-07
                                                                                                                                                                                                                                                     Query Match 12.5%; Score 25.8; I
Best Local Similarity 47.3%; Pred. No. 13;
Matches 78; Conservative 0; Mismatches
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EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-25
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-06-13
EARLIER FILING DATE: 1997-06-13
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EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER APPLICATION NUMBER: 60/047,502
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Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 46
US-09-149-476-114
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R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,889 R FILING DATE: 1997-08-22 R PILING DATE: 1997-08-22 R PILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,872 ILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 LICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: 60/047,612 LICATION NUMBER: 60/047,601 APPLICATION NUMBER: 60/043,314 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-08-22 1997-05-23 FILING DATE: 1997-05-23 1997-05-23 1997-05-23 1997-04-11 LING DATE: 1997-04-11 LING DATE: 1997-04-11 FILING DATE: 1997-04-11 1997-04-11

ER APPLICATION NUMBER: 60/043,576
ER PILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/047,501
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER APPLICATION NUMBER: 60/056,645 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 EARLIER APPLICATION NUMBER: 60/056,876 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,908 APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/056,862 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/048,964 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-04-1 FILING DATE: EARLIER DE LEAR DE LEAR DE LEARLIER DE LEA EARLIER EARLIER EARLIER ZEARLIER ZEARLIER ZEARLIER ZEARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1988-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1988-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/041,060
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/047,502
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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EARLIER APPLICATION NUMBER: 60/047,592

R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,311
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,671
R FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 PAPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,878 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 EARLIER APPLICATION NUMBER: 60/056,872 EARLIER FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23
APPLICATION UNMBER: 60/047,587
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: LING DATE: FILING DATE: LING DATE: BARLIER A
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                                                                                                                                                                                                                                                                                                                                                                          31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACTAAGC 90
                                                                                                                                                                                                                                                                             Query Match 12.5%; Score 25.8; DB 4; Length 1179; Best Local Similarity 47.3%; Pred. No. 13; Matches 78; Conservative 0; Mismatches 87; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WINGROVE, PETER
TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING
TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED
TITLE OF INVENTION: GABA-RECEPTOR SUBUNIT CDNA SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TITCACGACACTICCAAGGACGCCATACCGAACAAAGCAAGGIGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 675 TTAGGCCCGCCTCTGATGAATCAAGACCCTTCAAAGGTATATGT 719
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STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeg for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,330A
                 EARLIER APPLICATION UNBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER PEDILOCATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-06-13
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05-APR-1995
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APPLICANT: LE BOURDELLES, BEATRICE
APPLICANT: WHITING, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: T11091A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08417330A Patent No. 5719057 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,545
EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HAND, MARK
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LENGTH: 2191 base pairs
TYPE: , nucleic acid
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TITLE OF INVENTION: GAB!
TITLE OF INVENTION: GAB!
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-APR-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-417-330A-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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2695 GAAAİTIGCAAĞIİCIİTITIGAAİTİTCCIĞIACACITCIAAİTICGALTCATIAAIAIAAC 2636
                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                               30 TICTIGGICAATTICCAGGACACAGATGATICGGICCAAGAACAGGATAATAGAACTAAG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGAT 77
                                                                                                                                            12.5%; Score 25.8; DB 1; Length 2191; 60.9%; Pred. No. 17; Live 0; Mismatches 27; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.5%; Score 25.8; DB 3; Length 3077; Best Local Similarity 63.9%; Pred. No. 19; Matches 39; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/09410028 ; Patent No. 6107471
                                                           NAME/KEY: Coding Sequence
LOCATION: 214...1566
OTHER INFORMATION:
                                                                                                                                                                               42; Conservative
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (2707)..(2895)
US-09-410-028-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1160) .. (1300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (2414) .. (2506)
            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (389)..(454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (85)..(321)
                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                 249 GAACTCGAT 241
                                                                                                                                                                                                                                                                                90 CAACGCGAT 98
                                                                                                             US-08-417-330A-11
                                                                                                                                                                                                                                                                                                                                                                                 US-09-410-028-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
                                               FEATURE:
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                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 49
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Sequence 9, Application US/08500857A

Sequence 9, Application US/08500857A

Patent No. 5912156

GENERAL INFORMATION:
APPLICANT: OHATA, SHOZO
APPLICANT: BURNELL, JAMES N

TITLE OF INVENTION: ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME
TITLE OF INVENTION: ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME
TITLE OF INVENTION: AND RECOMBINANT VECTOR AND TRANSFORMED PLANTS CONTAINING
TITLE OF INVENTION: THE DNA
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: 8110 GATE HOUSE ROAD SUITE SOU EAST
CITY: FALLS CHURCH
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 3180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.4%; Score 25.6; DB 2; Length 318
Best Local Similarity 59.7%; Pred. No. 23;
Matches 43; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-195-814-1/c

| Sequence 1, Application US/08195814
| Patent No. 5547869
| Patent No. 5547869
| Patent No. 5547869
| Patent No. 5547869
| Patent No. 5547869
| Patent No. 5547869
| APPLICANT: BERGION, MAX; JOURDAN, MIREITTE, JOUSSET, APPLICANT: BRANCOISE XAVIERE
| TITLE OF INVENTION: NOVEL PLASMIDS | NUMBER OF SEQUENCES: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,857A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-2
TELEPONE: 703-205-8000
TELEFAX: 103-205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3180 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: 142..3006
US-08-500-857A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                            US-08-500-857A-9
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1151 TGATTAGTAGGTTGACCTCTGTTAAGTGAATTTCCAGGACCAAGATATTTATATACCGGGA 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TGGTATGGACGTATACGAGTTCTTGGTCAATTTTCCAGGACACAGATGATTCGGTCCAAGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N IS A OR C OR G OR T, WHEREIN N IS ZERO TO 130 NUCLEOTIDES IN LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N IS A OR C OR G OR T, WHEREIN N IS ZERO TO 50 NUCLEOTIDES IN LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 5910;
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Pred. No. 30;
0; Mismatches 24; Indels
                                                                                                          MEDLULUM ILES.

COMPUTER: INP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
CLASSIFICATION DATA:
APPLICATION NAMBER: 07/881,054
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/881,054
FILING DATE: 1-MAY-1992
APPLICATION NUMBER: 07/28,735
FILING DATE: 1-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
ATTORNEY/AGENT INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFAX: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5910

"WAD:
NITLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPODOPTERA LITTORALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: DENSOVIRUS OF JUNONIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: LARVAE
                                                                                               E: FLOPPY DISK
IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%;
62.5%;
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Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: DENSOVIRUS
                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY I
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OTHER INFORMATION:
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OTHER INFORMATION:
                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1657
                                  USA
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CELL TYPE: S:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                             10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAPLOTYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-195-814-1
                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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1091 ACAG 1088

RESULT 52

71 ACAG 74

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Sequence 1, Application US/07767135; Patent No. 5234811; Batch No. 5234811; GENERAL INFORMATION:
APPLICANT: Beutler, Ernest
APPLICANT: Sorge, Joseph A
TITLE OF INVENTION: An Assay for a New Gaucher Disease; ITLE OF INVENTION: Mutation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of STREET: 3366 No. 5234811th Torrey Pines Court, Suite 240
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92037
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/767,135
FILING DATE: 19910927
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: intron
LOCATION: 612..979
OTHER INFORMATION: /function= "Intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1068..1619
OTHER INFORMATION: /function= "Intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1812..1934
OTHER INFORMATION: /function= "Intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 1935..2081
OTHER INFORMATION: /product= "Exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 356..611
OTHER INFORMATION: /product= "Exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATONNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0422P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7620 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 1620..1811
OTHER INFORMATION: /product= "Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 980..1067
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                       S
US-07-767-135-1
                                                                                                                                                                                                                                                                                                       STATE:
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5395 GAGTGTGCGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGCCACAGCATCATCACGGT 5454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GAGTICTIGGICAAITICCAGGACACAGATGATICGGICCAAGAACAGGATAATAGAACT 86
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NAME/KEY: intron
LOCATION: 2082..3046
OTHER INFORMATION: /function= "Intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 6503..6596
OTHER INFORMATION: /function= "Intron 10"
                                                                                                                                                                                                  LOCATION: 3181..3390
OTHER INFORMATION: /function= "Intron 5"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intron
LOCATION: 4355..5227
OTHER INFORMATION: /function= "Intron 7"
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LOCATION: 6017..6385
OTHER INFORMATION: /function= "Intron 9"
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OTHER INFORMATION: /function= "Intron 6"
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; LOCATION: 6597..7245
.: OTHER INFORMATION: /function= "Exon 11"
US-07-767-135-1
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OTHER INFORMATION: /function= "Intron
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                                                                                                NAME/KEY: exon
LOCATION: 3047..3180
OTHER INFORMATION: /product= "Exon 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /product= "Exon
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LOCATION: 3391..3563
OTHER INFORMATION: /product=
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LOCATION: 4117..4354
OTHER INFORMATION: /product=
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LOCATION: 5853..6016
OTHER INFORMATION: /product=
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LOCATION: 6386..6502
OTHER INFORMATION: /F
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NAME/KEY:
LOCATION:
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Sequence 1. Application US/07841652
Sequence 1. Application US/07841652
Sequence 1. S26459
GENERAL INFORMATION:
APPLICANT: Bentler, Ernest
TITLE OF INVENTION: GAUCHER'S DISEASE: DETECTION OF A NEW
TITLE OF INVENTION: MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
CORRESPONDENCES: ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5266459th Torrey Pines Road, TPC 8
CITY: La Jolia
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,652
FILING DATE: 19920224
CLASSIFICATION: 435
PCICASIFICATION DATA:
APPLICATION NUMBER:
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LOCATION: 1812..1934
OTHER INFORMATION: /function= "Intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: intron
LOCATION: 612..979
OTHER INFORMATION: /function= "Intron 1"
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LOCATION: 1068..1619
OTHER INFORMATION: /function="Intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 980..1067
OTHER INFORMATION: /product= "Exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1620..1811
OTHER INFORMATION: /product= "Exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BIGGAM, DOUGLAS A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0670P
TELECOMUTICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 76.20 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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LOCATION: 1620..1811
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OTHER INFORMATION:
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5455 AAGCCACCCCAGTCTCCTGCAAAAGCAGACCTCAGACCTCTTACTAGTTTCACCAA 5514
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LOCATION: 6503..6596
OTHER INFORMATION: /function= "Intron 10"
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LOCATION: 5453.5852
OTHER INFORMATION: /function= "Intron 8"
                                                                NAME/KEY: intron
LOCATION: 2082..3046
OTHER INFORMATION: /function= "Intron 4"
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LOCATION: 4355..5227
OTHER INFORMATION: /function= "Intron 7"
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OTHER INFORMATION: /function= "Intron 9"
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OTHER INFORMATION: /function= "Intron 6"
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OTHER INFORMATION: /product= "Exon 10"
                                                                                                                                                                                                                                                                             LOCATION: 3181..3390
OTHER INFORMATION: /function= "Intron
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LOCATION: 5228..5452
OTHER INFORMATION: /product= "Exon 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 4117..4354
OTHER INFORMATION: /product= "Exon 7"
                   OTHER INFORMATION: /product= "Exon 4"
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OTHER INFORMATION: /product= "Exon 6"
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OTHER INFORMATION: /product=
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LOCATION: 5853..6016
OTHER INFORMATION: /product=
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6597..7245
LOCATION: 1935..2081
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; LOCATION:
US-07-841-652-1
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RESULT 54
US-09-784-316-3/c
is Sequence 3, Application US/09784316
is Sequence 3, Application US/09784316
is Patent No. 6461843
is GENERAL INFORMATION:
is APPLICANT: WEI, Ming-Hui et al.
itTLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
itTLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
itTLE OF INVENTION: THEREOF
itTLE OF INVENTION: THEREOF
itTLE OF INVENTION: THEREOF
itTLE OF INVENTION: THEREOF
itTLE OF INVENTION: THEREOF
itTLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
itTLE OF INVENTION NUMBER: US/09/784,316
itTLE NUMBER OF SEQ ID NOS: 5
itTLE OF INVENTION NUMBER: ACID NOS: 5
itTLE OF INVENTION NUMBER: ACID NOS: 5
itTLE OF INVENTION NUMBER: ACID NOS: 5
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5515 AGACTGACAGAAGCCCTTCCTGTCCAGCTTTCCCCAGCTAGCCTGCCCTTTTGAGC 5570
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.4%; Score 25.6; DE
Best Local Similarity 59.7%; Pred. No. 82;
Matches 43; Conservative 0; Mismatches
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Patent No. 592853
GENERAL INFORMATION:
APPLICANT: HANSBURY, MICHAEL J
APPLICANT: JACKSON, JEFREY R
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
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; OTHER INFORMATION: n = A, T, C or G
US-09-784-316-3
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NAME: PRESTIA, PAUL F
'REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: RATWER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1997
N: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 44586 AGAACAATGTAA 44575
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 65042
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US-08-892-715-1
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STATE:
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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 25.4; DB 2; Length 1632; 64.4%; Pred. No. 20; tive 0; Mismatches 21; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  99 ACAATTIGGGIGGATIGGCAACAAACTICCIGIGACTAACAGGICCAIAGTITITICACG 157
                                                                                                                                                                                                                                                                                                                                                                                                                               918 ACAAGCAGTGAAGACCGACAACAACTGCTCCTGGAAAACCGGTCCAAATTTCTTCAGG 976
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                                                                                                                                                                                                                                                                                      Query Match 12.3%; Score 25.4; DB 2; Length 1632; Best Local Similarity 64.4%; Pred. No. 20; Matches 38; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09145947
Patent No. 5925539
GENERAL INFORMATION:
APPLICANT: HANSBURY, MICHAEL J
APPLICANT: JACKSON, JEFFREY R
ITILE OF INVENTION: A HUMAN PELOTA HOMOLOG
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS;
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,947
FILING DATE: 02-SEPT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GH-70144-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,715
FILING DATE: 15-JUL-1997
ATTORNEY/ACENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                 TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1632 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.3%
Best Local Similarity 64.4%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-892-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΡA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-145-947-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
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FRACELL NO. 0.30-1446

APPLICANT: JACOBSON, Myron K.

APPLICANT: JACOBSON, Elaine L.

APPLICANT: JACOBSON, Elaine L.

APPLICANT: JACOBSON, Elaine L.

APPLICANT: JACOBSON, Elaine L.

APPLICANT: JA, Jean-Christophe

APPLICANT: LIN, Winston

TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ

TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE

TITLE OF INVENTION: HAD 201

CURRENT PELING DATE: 1999-04-30

EARLIER APPLICATION NUMBER: 60/083,768

EARLIER APPLICATION NUMBER: 60/083,768

EARLIER PILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 38

SEQ ID NOS: 38

SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) EN TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVATURE OF INVENTION: THEREWITH FILE REFERENCE: NIAD 201
CURRENT APPLICATION NUMBER: US/09/511,477
CURRENT FILING DATE: 2000-02-23
PRIOR FILIAGE DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                  25 ACGAGITCITGGICAAITICCAGGACACAGAIGATICGGICCAAGAACAGGATAATAGAA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 29793;
                                                                                                                   DB 4; Length 3097;
                                                                                                                                                                    26; Indels
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                                                                                                                 Query Match
12.3%; Score 25.4; DE
Best Local Similarity 61.2%; Pred. No. 27;
Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%; Score 25.4; I 64.4%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 38, Application US/09302812B ; Patent No. 6333148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 38, Application US/09511477; Patent No. 6337202; GENERAL INFORMATION: APPLICANT: JACOBSON, Myron K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: AME, Jean-Christophe
APPLICANT: LIN, Winston
; LENGTH: 3097
; TTYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.35
Best Local Similarity 64.45
Matches 38; Conservative
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US-09-511-477-38/c
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LENGTH: 297
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Sequence 11, Application US/09228986

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ACAATTIGGGIGGATIGGCAACAACTICCIGIGACTAACAGGICCATAGTITITCACG 157
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12.3%; Score 25.4; DB 4; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0
                                                                                    Sequence 1, Application US/09265642

Batent No. 634284

GENERAL INFORMATION:
APPLICANT: JACKSON, JEFFREY R.
APPLICANT: HANSBURY, MICHAEL J.
TITLE OF INVENTION: HUMAN PELOTA HOMOLOG
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STRRET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/265,642
FILING DATE: 10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/09/265,642
10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,947
FILING DATE: 02-SEP-1998
APPLICATION NUMBER: 08/892,715
FILING DATE: 15-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REPREDICE/DOCKET NUMBER: GP-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 58
US-09-228-986-11/c
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                                                                               US-09-265-642-1
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORNATION:
APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JAN, Winston
TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) EN
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION: THEREWITH
TITLE OF INVENTION: THEREWITH
TITLE OF INVENTION: THEREWITH
TITLE OF INVENTION: THEREWITH
TITLE OF INVENTION: 000-02-23
PRIOR PELLING DATE: 2000-02-23
PRIOR PELLING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                    ;
0
                                                                                                                                                                                                                 12.3%; Score 25.4; DB 4; Length 29793; 64.4%; Pred. No. 69; tive 0; Mismatches 21; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3695 TICGIAGICTITCTCCTGTAAAAAGATGATAATGTICAAGTAATAAAAAACTATAACTAA 3637
                                                                                                                                                                                          30 ITCTIGGICAATITCCAGGACACAGAIGATICGGICCAAGAACAGGATAATAGAACTAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 TICTIGGICAATTICCAGGACACAGATGATICGGICCAAGGAACAGGATAATAGAACTAA 88
                                                                                                                                                 0;
                                                                                                 DB 4; Length 29793;
                                                                                            12.3%; Score 25.4; DB 4; Length 29°64.4%; Pred. No. 69;
tive 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CWRRENT APPLICATION DATA: PLING DATE: VS/08/425,315 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE Lowe, Price, LeBlanc and Becker
STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08425315
Patent No. 5545820
GENERAL INFORMATION:
APPLICANT: Gatehouse, Angharad
APPLICANT: Hilder, Vaughan
APPLICANT: Peumans, Willy
APPLICANT: Peumans, Willy
APPLICANT: INSECTICIDAL PROTEINS
ITTLE OF INVENTION: INSECTICIDAL PROTEINS
UNMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09511507
Patent No. 6395543
ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Caenorhabaditis elegans
                                                                                         Query Match
Best Local Similarity 64.44
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.44
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 99 Canal
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                             RESULT 61
US-09-511-507-38/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEO ID NO 38
LENGTH: 29793
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                              ; FEALUNE.
US-09-511-477-38
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9 CATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: 1..67
OTHER INFORMATION: /note= "Putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 69.382
OTHER INFORMATION: /note= "Putative mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
; LOCATION: 488..610
; OTHER INFORMATION: /note= "3' untranslated region"
US-08-425-315-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Putative C-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 63
US-08-716-190-1/C
Sequence 1, Application US/08716190
Sequence 1, Application US/08716190
RENERAL INFORMATION:
APPLICANT: REGORDERAN, Irene
APPLICANT: RESCHENSON, Walter
APPLICANT: RATEHOUSE, Angharad Margaret
APPLICANT: ROSCOE
APPLICANT: ROSCOE
ITTLE OF INVENTION: NEWATICIDAL PROTEINS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: LOWE, PRICE, LEBLANC & BECKER
99 Canal Center Plaza, Suite 300
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,841
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mills, Demetra J.
REGISTRATION NUMBER: 34,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GAACAGGATAATAGAACTAAGCAACG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GTACAGGATATTATTACTCAGGCAAG 57
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 26.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Galantus nivalis
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 383..487
OTHER INFORMATION: /not
OTHER INFORMATION: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: 68..382
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
                                                                                                                                                                                                                                      TELEFAX: (703) 684-112
TELEX: 82-4425
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: LOWE, PRICE
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
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101 AATTIGGGTGGATIGGCAACAAACTICCTGTGACTAACAGGTCCATAGTTTTTCACGACA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AAGTTGGACTGATTGGTCCTGACCTTCCTTTCACTAACAACTACGGTGTTTGGGAAGATG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Degenerate polynucleotide sequence of zapop3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.2%; Score 25.2; DB 4; Length 1272; Best Local Similarity 60.0%; Pred. No. 21; Matches 42; Conservative 0; Mismatches 28; Indels 0.
COUNTRY: USA
ZIP: 95516
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
COMPUTER: IBM PC
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: Microsoft Word For Windows 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,758
FILING DATE: 8-8-97
CLASSIFICATION 1800
PRIOR APPLICATION NUMBER: 60/024,145
FILING DATE: 8-9-96
ATTORNEY/AGATI INFORMATION:
NAME: Donna E Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 35,924
REFERENCE/DOCKET NUMBER: 35,924
REFERENCE/DOCKET NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 122-1
TELEPONNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEPHONE: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
CFOUNTENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Venezia, Domenick
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
FILE REFERENCE: 98-41
CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258
EARLIER APPLICATION NUMBER: US 60/108,258
SARLIER FILING DATE: 1998-11-12
NUMBER OF SQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (1)...(2169); CHER INFORMATION: n = A,T,C or GUS-09-434-408-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-434-408-3/c
; Sequence 3. Application US/09434408
: Patent No. 6446697
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA
US-08-908-758-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 CTTCCAAGGA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AGTTCAACGA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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Patent No. 6429356
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING CAROTENOID COMPOUNDS AND SPECIALLY OIL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start= 383
/product= "Putative C-terminal peptide P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 610;
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12.2%; Score 25.2; DB 3; Length 610
Best Local Similarity 55.8%; Pred. No. 16;
Matches 48; Conservative 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Putative mature protein
p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig_peptide
LOCATION: 2.67
OCHER INFORMATION: /product= "Putative signal peptide
OTHER INFORMATION: P"
           COMPUTER READABLE FORM:

MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,190
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PRICE, Robert L
REGISTRATION NUMBER: 22,685
REFRENCE/DOCKET NUMBER: 22,685
TELECOMMUNICATION INFORMATION:
TELEPRAX: 703-684-1111
TELEPRAX: 703-684-1111
TELEPRAX: 703-684-1111
TELEPRAX: 703-684-11124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 610 base pairs
TYPE: nuclei caid
STRANDENESS: double
STRANDENESS: double
STRANDENESS: double
TOWN FOR THE STRANDENESS: Gouble
STRANDENESS: Gouble
TOWN FOR THE STRANDENESS: Gouble
TOWN FOR THE STRANDENESS: GOUBLE
TOWN FOR THE STRANDENESS: GOUBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GTACAGGATATTATTACTCAGGCAAG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Galanthus nivalis
IMMEDIATE SOURCE:
CLONE: LECGNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 68..382
OTHER INFORMATION: /pr
OTHER INFORMATION: P"
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 2..487
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: 3'UTR
LOCATION: 488..610
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STREET: Low.
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US-08-908-758-3
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Patent No. 6008322
                                                                                                                     1471 TNARYTCNARYTGNGTNARYTGNARNARYTCNGTYTCDATNARYTTDATYTGNSWNCKDA 1412
                                                                                                                                                                              65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAAC 124
                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                         5 GAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
                                                                                                                                                                                                                                                                                               12.2%; Score 25.2; DB 4; Length 2169; 26.7%; Pred. No. 27; tive 34; Mismatches 92; Indels 0
                                                                                                                                                                                                                                                                          125 TTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 CAAGAGTTGTTCTCGAAACATTCAAACACGCCACACCCCACACTCGCCAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.1%; Score 25; DB 2; Length 892; Best Local Similarity 69.4%; Pred. No. 22; Matches 34; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CCATAGTITITCACGACACTICCAAGGACGCCATACCGAACAAAGCAAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUMPOTER: 14MP 57/24

OPERATING SYSTEM: MS.DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGBAT INPORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-460-529B-1/C

Sequence 1, Application US/08460529B

Patent No. 5994103

GENERAL INFORMATION:

APPLICANT: OLSEN, ET AL.

ITILE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: CRECHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD
                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5 INCH DISKETTE
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; Sequence 1, Application US/08831132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                892 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: LINEAR; MOLECULE TYPE: cDNA
US-08-460-529B-1
                     Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6 BECKI
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07068
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  Query Match
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 caagagirgrictcgaaacartcaaacacacacacacacacacacacag 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CCATAGITITICACGACACTICCAAGGACGCCATACCGAACAAGCAAG 191
                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lok, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
           APPLICANT: Kuestner, Rolf E.
APPLICANT: Conklin, Darrell C.
APPLICANT: Buddle, Michele
APPLICANT: Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
                                                                                                                                                          E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
EEFERENCE/DOCKET VUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kuestner, Rolf E. Conklin, Darrell C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-416-150-1/c
; Sequence 1, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 206-7.2
TELEPHONE: 206-442-6678
TOTAL TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
1..72
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 34, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
GENERAL INFORMATION:
APPLICANT: Kuestne
APPLICANT: Conklin
                                                                                                                                                                                               Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                 98102
                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY:
, LOCATION:
US-08-831-132-1
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                           STREET:
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ADDRESSEE: ZymoGenetics, Inc.

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; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-134-001C-850
                                                                                                                                                                                                                       64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCAACAAA 123
                                                                                                                                                                                                                                                                      405 TCTAACATGTGTAGAATAGCTTTTGAGCCACTTTATTAATTTTAAGTGGGTGTCCAAAAAC 346
                                                                                                                                                                                                                                                                                                                        124 CTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAAC 183
                                                                                                                                                                                                                                                                                                                                                                         345 AATATATCCTCTTCACTCATGATTTGACCAATGTCTAATTGGTCTCCATTTCTTAC 286
                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
8.08-08-313-075A-29/C
5 Sequence 29, Application US/08313075A
6 SEQUENCE 29, Application US/08313075A
6 FAREAL INFORMATION:
7 APPLICANT: Holton, Timothy A.
7 APPLICANT: Tanaka, Yoshikazu
7 TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
7 TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
7 TITLE OF SEQUENCES: 58
                                                                                                                     Query Match 12.1%; Score 25; DB 4; Length 1014; Best Local Similarity 48.9%; Pred. No. 23; Matches 67; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTRACTION CATTERN: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A FILING DATE: 30-NOV-1994 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEYX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31,346
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                                                                                                                                                                                                                                                                                                                                                                                                                           184 AAAGCAAGGTGTTATTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 ATGATAAACAGTTAATA 269
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LENGTH: 1665 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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: U.S.A.
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NAME/KEY: unsure
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Sequence 850, Application US/09134001C

Sequence 850, Application US/09134001C

Sequence 850, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: USCID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APLICATION NUMBER: US 60/065,779

PRIOR FILING DATE: 1997-10-08

PRIOR FILING DATE: 1997-08-14

RECORD ACID NOS: 5674

SEQ ID NOS: 5674

SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 25; DB 4; Length 906; 69.4%; Pred. No. 22; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 CCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAAGCAAG 191
                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,150
FILING DATE: 11-Oct-1999
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,132
     STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..906
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 206-442-6678
TELEPAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
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                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
                                 Seattle
                                                      STATE: WA
COUNTRY: USA
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                                                                                                     ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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US-09-134-001C-850/c
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FEATURE:

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                                                                                                                                                                                                                                                                       87 AAGCAACGCGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCAT 146
                                                                                                                                                                             27 GAGTICTIGGICAAITTICCAGGACACAGAIGATICGGICCAAGAACAGGAIAATAGAACT 86
                                                                                                                                         0; Gaps
                                                                                          Score 25; DB 1; Length 1665;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.1%; Score 25; DB 1; Length 1666; Best Local Similarity 48.3%; Pred. No. 28; Matches 70; Conservative 0; Mismatches 75; Indels
                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
                                                                       12.1%; Scor. 48.3%; Pred. No. 20, ... 0; Mismatches '...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                              147 AGTTTTTCACGACACTTCCAAGGAC 171
                                                                                                                                                                                                                                                                                                                                                                                                         189 ATTTTTGGCTAAATCTCTAAGGAC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/07912900
Patent No. 5349125
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1666 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                             Best Local Similarity 48.33
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 CITY: Garden City STATE: New York
                       3..1432
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-912-900-24/c
                            ,
US-08-313-075A-29
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                     LOCATION:
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                                                                                          Query Match
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27 GAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAACT 86

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75; Indels

0; Mismatches

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  250 CAGGAGAAGTAACTACAACGGCAGAAATTTTACCTAGTTGAAGGTGCATAATTGGTCCAT 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 caggagaagtaactacaacggcagaattttacctagttgaaggtgcafaattggtccaf 191
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                                                                                                                                                                                                                                                                           APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diana R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                           147 AGTITITCACGACACTICCAAGGAC 171
                                                                                            190 ATTITITGCTAAATCTCTAAGGAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AGTITITCACGACACTICCAAGGAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ATTTTTTGGCTAAATCTCTAAGGAC 166
                                                                                                                                                                                                         Sequence 24, Application US/08285309
Patent No. 5569832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INPORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 863
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-285-309-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1666 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                   US-08-285-309-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                RESULT 72
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0; Mismatches 30; Indels
                                                                                                                               NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION Elease #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /product= "E-CYCLASE FROM A. OTHER INFORMATION: THALIANA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-063-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
CUNNINGHAM JR., FRANCIS X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1860 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                APPLICANT: SUN, ZAIREN TITLE OF INVENTION: GEN TITLE OF INVENTION: MET
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 ATGAATTCAATGA 575
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STRANDEDNESS:
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US-07-869-933-22/c
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   APPLICANT:
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                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwina C.

APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION: HYDROXYLASE AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/502,046

FILING DATE: 14-JUL-1995

CLASSIFICATION #00

PRIOR APPLICATION #00

PRIOR APPLICATION #00

PRIOR APPLICATION #00

PRIOR APPLICATION #00

ATTORNEY/AGENT INFORMATION:

NAME: DidGiglio, Frank S.

REGISTRATION NUMBER: 8633Z

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4366

TELEPHONE: (516) 742-4366

TELEPHAX: (516) 742-4366

TELEPHAX: (516) 742-4366

TELEPHAX: (516) 742-4366

TELEPHAX: 166 DASE PAIRS

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1666 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: U.S.A. ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/M
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                                                                                                                                             Sequence 24, Application US/08502046 Patent No. 5861487
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; Sequence 1, Application US/08624125
Patent No. 574434
; GENERAL INFORMATION:
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Sequence 22, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET,
APPLICANT: ATLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN 98 TACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACG 157 503 TAAAAGTTGGACTCATTGGTCCAGATCTTCCTTTTACTAACAATTACGGTGTTTGGGAAG 562 GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES 0; Gaps / Match 12.1%; Score 25; DB 1; Length 1860; Local Similarity 58.9%; Pred No. 30;

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111.807 Million cell updates/sec
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Sequence 10, Sequence 7, Al
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Sequence 56,
Sequence 38,
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Sequence 4, 1
Sequence 6, A
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Sequence 4,
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Sequence 2
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Sequence 2
Sequence 1
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Sequence 1
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                                                                                                                                                           February 11, 2003, 08:36:01 ; Search time 15 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
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                                                                                                                                                               APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: OKAMA, NORIYUKI
APPLICANT: YOSHIDA, MASAYA
APPLICANT: AVGASTA, SARAB
APPLICANT: AVGASTA, SARAB
APPLICANT: AVAI, AKIRA
TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,437
FILING DATE: 2-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: UP PCT/JP93/01133
FILING DATE: 11-AUG-1992
PRIOR APPLICATION NUMBER: UP 234085/1992
ATOMAN APPLICATION NUMBER: JP 234085/1992
ATOMANEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
ALIGNMENTS
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    Sequence 2, Application US/08379437
Patent No. 5734014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMULAL.
TELEPHONE: 703-413-220
TELEFAX: 703-413-220
TELERAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TOWGTH: 57 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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MEDIUM TYPE: Floppy of
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              TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%; Score 324; DB 1; Length 57; 98.2%; Pred. No. 2.8e-28; Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/379,437
FILING DATE: 27-MAR-1995
CLIASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP PCT/JP93/01133
FILING DATE: 11-AuG-1992
PRIOR APPLICATION DATA:
FILING DATE: 11-AuG-1992
APPLICATION NUMBER: UP 234085/1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 98.28
Marches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-379-437-4
APPLICANT: KAJI, AKIRA
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3Y: linear
                                                                                                                                      ARLINGTON
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PatentIn Release #1.0, Version #1.30

SOFTWARE:

Sequence 4, Application US/08379437
Patent No. 5734014
GENERAL INFORMATION:
APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: OKAMA, NORYTWKI
APPLICANT: YOSHIDA, MASAYA
APPLICANT: AMAGAYA, SAKAE

US-08-379-437-4

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amino acid
                                                                                                                    amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-379-437-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AQEPVKGPVSTKPGSCPIILIRCAVLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 98.8%; Score 323; DB 1; Length 57; Best Local Similarity 98.2%; Pred. No. 3.6e-28; Matches 56; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,437
FILING DATE: 27-MAR-1995
CLASSIFICATION NUMBER: UP PCT/JP93/01133
APPLICATION NUMBER: UP PCT/JP93/01133
FILING DATE: 11-AUG-1992
ATPONEY/AGENT INPOMBER: 224,618
FEGISTRATION NUMBER: 24,618
FEGISTRATION NUMBER: 24,618
TELECOMMUNICATION NUMBER: 24,618
TELECOMMUNICATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08379437
Patent No. 5734014
GENERAL INFORMATION:
APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: YOSHIDA, MASAYA
APPLICANT: AMAGAYA, SAKAE
APPLICANT: AMAGAYA, SAKAE
TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
WINNER OF SEQUENCES: 16
             CARACATION NUMBER: US/08/379,437
FILING DATE: 27-MAR-1995
CLASSIFICATION 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP93/01133
FILING DATE: 11-AUG-1992
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-220
TELEPAX: 703-413-220
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-379-437-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS ADDRESSE: OBLON, SI
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GY: linear
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STATE:
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TERENEY, 703-431-220

TERENEY, 703-431-220

TERENEY, 704-431-220

TERENEY, 704-68 SO LPAT UB

SEQUENCE CHARACTERISTICS

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US-09-326-039-7
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                                                                                    1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                        1 AQEPVKGPVSTKPGSCPIILIRCAXLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                        US-08-761-248B-10

Sequence 10, Application US/08761248B

Patent No. 595873.

GENERAL INFORMATION:

APPLICANT: ROWLEY, DAVID R.

TITLE OF INVENTION: PACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
ch 98.2%; Score 321; DB 1; Length 57; 1 Similarity 98.2%; Pred. No. 5.9e-28; 56; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 76.1%; Score 249; DB 2; Length 42; Best Local Similarity 100.0%; Pred. No. 2.2e-20; Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 CPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CONKLIN, Darrell
TITLE OF INVENTION: Disulfide Core Polypeptides
FILE REFERENCE: 98-13
CURRENT APPLICATION NUMBER: US/09/326,039
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09326039
Patent No. 6239254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34(
TELECOMMUNICATION:
TELEPHONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (713)951331
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 77002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-761-248B-10
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                                          Matches
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Gaps
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                                                                                                                                                                                                                                                                              Length 40;
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43.7%; Score 143; DB 3; Length 60;
Best Local Similarity 48.2%; Pred. No. 7-609;
Matches 27; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08483503A
Patent No. 6017880
GENERAL INFORMATION:
APPLICANT: Bisenberg, Stephen
APPLICANT: Wahl, Sharon M.
APPLICANT: Thompson, Robert C.
APPLICANT: Dripps, David J.
TITLE OF INVENTION: INHIBITION OF RETROVIRUS INFECTION
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                      Query Match 71.3%; Score 233; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       18 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                  1 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 40
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CURRENT FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/088,136
EBARLIER FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04.
TELECOMMUNICATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-400-...
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 60 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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US-08-483-503A-1
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Best Local Similarity
Matches 27; Conserva
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US-07-963-538B-4
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                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MATSUMOTO, YOHICHI
APPLICANT: TAKBUCHI, AKIKO
TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
TITLE OF INVENTION: TECHNOLOGY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                       3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                    2 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-0CT 1992
CLASSIFICATION DATA:

PELLING DATE: 20-0CT 1992
PRIOR APPLICATION NUMBER: US/07/843,359
FILING DATE: 25-FEB-1992
PRIOR APPLICATION NUMBER: US 07/408,483
FILING DATE: 25-AUG-1989
PRIOR APPLICATION NUMBER: US 07/408,483
FILING DATE: 22-AUG-1999
PRIOR APPLICATION NUMBER: UP 4-212399
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 4-212398
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 3-355553
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:
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FILING DATE: 28-DEC-1987
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: TEJN-005/02US
TELECHONE: 415-843-5070
TELEPRA: 415-843-5070
TELEPRA: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: COOLEY GODWARD LLP
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    Sequence 4, Application US/07963538B Patent No. 5851983
                                                                                                                                                                                                                                                                                                                                       OHTSUKA, EIKO
IMAIZUMI, ATSUSHI
WATANABE, KUNIHITO
SUGA, TETSUYA
MATSUMOTO, YOHICHI
TAKEUCHI, MAKIKO
                                                                                                                                                                                                                                                    SUGIYAMA, TAKASHI
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MASUDA, KENICHI
OKADA, MASAHIRO
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amino acid
GY: linear
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SUGIYA
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                               US-07-963-538B-4
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
TITLE OF INVENTION: Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STREET: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                          49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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48.2%; Pred. No. 1.5e-08;
ttive 4; Mismatches 23; Indels
Query Match
Best Local Similarity 48.2%; Pred. No. 1.2e-08;
Matches 27; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Complete amino acid sequence of human SLPI NAME/KEY: (antileukoprotease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NOWBER: US/08/304,051
FILING DATE: 12.5ept-1994
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION BATA: NO. 563327e
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: MWH 322
TELEFONDENCE/DOCKET NUMBER: MWH 322
TELEPHONE: (200) 937-2712
                                                                                                                                                                                                                                                          RESULT 10
US-08-304-051-21
Sequence 21, Application US/08304051
; Patent No. 5633227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEEX: (2.03) 937-2795
TELEX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
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VOLUME: 1
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NAME/KEY: Complete amino acid sequence of human SLPI
NAME/KEY: (antileukoprotease).
PUBLICATION INFORMATION:
AUTHORS: Heinzel, R., Appelhans, H., Gassen, G.,
AUTHORS: Seemuller, U., Machleidt, W., Fritz, H., and Steffens, G.
TITLE: Molecular cloning and expression of cDNA for
TITLE: human antileukoprotease from cervix uterus
JOHENAL: European Journal of Biochemistry
                            74, DPVDTFNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 129
3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                                                                                                                                                 PCT-US95-11445-21
Sequence 21, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
APPLICANT: Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
43.7%; Score 143; DB 5; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.5e-08;
Matches 27; Conservative 4; Mismatches 23; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macinicsh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MWH 322P1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: MWH 3221
TELEPHONE: (203) 937-5492
TELEPHONE: (203) 937-5492
TELEPHONE: (203) 937-5492
TELEPHONE: GRAY DOS: 21: SEQUENCE OF SEQUENCE: 1100 NO: 21: SEQUENCE OF SEQUENCE: 1100 NO: 21: SEQUENCE OF SEQUENCE: 1100 NO: 21: SEQUENCE OF SEQUENCE: 1100 NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO CORIGINAL SOURCE: ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                RESULT 11
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APPLICANT: MATSUMOTO, YOHICHI
APPLICANT: TAREUCHI, AKTKO
TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
TITLE OF INVENTION: TECHNOLOGY
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.1%; Score 141; DB 2; Length 53; 49.0%; Pred. No. 1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-0CT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/843,359
FILING DATE: 25-FEB.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,483
FILING DATE: 22-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,483
FILING DATE: 22-AUG-1989
PRIOR APPLICATION NUMBER: US 07/408,483
FILING DATE: 22-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: UF 4-212399
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-212398
FILING DATE: 17-UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-35553
FILING DATE: 24-DEC-1991
PRIOR APPLICATION NUMBER: UP 62-330219
FILING DATE: 28-DEC-1991
PRIOR APPLICATION NUMBER: UP 62-330219
FILING DATE: 28-DEC-1987
APPLICATION NUMBER: UP 62-330219
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: 30,092
REFERENCE/DOCKET NUMBER: TEJN-005/02US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: COOLEY GODWARD LLP
: FIVE PALO ALTO SQUARE, 4TH FLOOR
PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            ; Sequence 1, Application US/07963538B; Patent No. 5851983
                                                                                                                                                                                                           OHTSUKA, EIKO
IMAIZUMI, ATSUSHI
WATANABE, KUNIHITO
SUGA, TETSUYA
MATSUMOTO, YOHICHI
                                                                                                                SUGIYAMA, TAKASHI
KAMIMURA, TAKASHI
MASUDA, KENICHI
OKADA, MASAHIRO
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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415-857-0663
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                                                                                        GENERAL INFORMATION:
APPLICANT: SUGIYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94306-2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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RESULT 12
US-07-963-538B-1
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APPLICANT:
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APPLICANT:
                                                                                                                                      APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Best Local Similarity

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TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE TITLE OF INVENTION: TECHNOLOGY NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 3.2e-08;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                                                                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM:

OPERATION OF PACEDICAL MELOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-0CT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/843,359
FILING DATE: 25-FEB-1992
PRIOR APPLICATION NUMBER: US 07/408,483
FILING DATE: 25-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/408,483
FILING DATE: 27-MG-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-212399
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 17-JUL-1992
FILING DATE: 17-JUL-1992
PRIOR APPLICATION NUMBER: JP 4-212398
FILING DATE: 17-JUL-1992
PRIOR APPLICATION NUMBER: JP 62-330219
APPLICATION NUMBER: JP 62-330219
APPLICATION NUMBER: JP 62-330219
APPLICATION NUMBER: JP 62-330219
                                                                                                                                                                          E: COOLEY GODWARD LLP
FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 62-330219
FILING DATE: 28-DEC-1987
ATTORNEY AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: TEJN-005/02US
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07963538B; Patent No. 5851983; GENERAL INFORMATION: GAPLICANT: SUGIYAMA, TAKASHI APPLICANT: KAMIMURA, TAKASHI
                  MATSUMOTO, YOHICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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51.1%;
                                            TAKEUCHI, AKIKO
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415-857-0663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
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SUGA, TETSUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                 ZIP: 94306-2155
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                         PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-963-538B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-963-538B-3
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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Gaps
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                                                                                                                                                                                               Sequence 9, Application US/08761248B
Patent No. 5958735
GENERAL INFORMATION:
TITLE OF INVENTION: URCGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                              8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                      2 PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
  22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPRVMIYCPARHPPNKCTSDYDCPKPQKCCPGYCGKQCYQPE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/07963538B Patent No. 5851983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUGIYAMA, TAKASHI
KAMIMURA, TAKASHI
MASUDA, KENICHI
OKADA, MASAHIRO
OHTSUKA, BIKO
IMAIZUMI, ATSUSHI
WATANABE, KUNIHITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Turley, Charles P
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: TX
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
    Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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APPLICANT: SUGIYA
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APPLICANT:
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APPLICANT:
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US-07-963-538B-3
24;
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    Matches
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41.6%; Score 136; DB 2; Length 50;
Best Local Similarity 51.1%; Pred. No. 3.3e-08;
Matches 23; Conservative 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CLESSIPTION NUMBER: US/07/963,538B
FILING DATE: US-0CT-1992
CLESSIPTION: DATA:
APPLICATION NUMBER: US 07/843,359
FILING DATE: 25-REB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,483
FILING DATE: 22-MG-1899
PRIOR APPLICATION NUMBER: UP 4-212399
FILING DATE: 17-UL-1992
PRIOR APPLICATION NUMBER: UP 4-212399
FILING DATE: 17-UL-1992
PRIOR APPLICATION NUMBER: UP 4-212399
FILING DATE: 17-UL-1992
PRIOR APPLICATION NUMBER: UP 3-355553
FILING DATE: 24-DEC-1991
PRIOR APPLICATION NUMBER: UP 6-230219
PRIOR APPLICATION NUMBER: UP 6-230219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 47
                                                                                                                                                                                                                                                                                                   SEE: COOLEY GODWARD LLP
: FIVE PALO ALTO SQUARE, 4TH FLOOR
PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEJN-005/02US
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FILING DATE: 28-DEC-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30,092
                                                                 IMAIZUMI, ATSUSHI
WATANABE, KUNIHITO
SUGA, TETSUYA
MATSUMOTO, YOHICHI
TAKEUCHI, AKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TEL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5070
MASUDA, KENICHI
OKADA, MASAHIRO
OHTSUKA, EIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 50 amino acids
                                                                                                                                                        APPLICANT: TAKEUCHI, AK
TITLE OF INVENTION: ELA
TITLE OF INVENTION: PRO
TITLE OF INVENTION: TEC
NUMBER OF SEQUENCES: 36
CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306-2155
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide

US-07-963-538B-2
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                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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RESULT 16 US-08-483,503A-3

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3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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44.6%; Pred. No. 5e-08;
ttive 4; Mismatches 25; Indels
                                                                         APPLICANT: Eisenberg, Stephen
APPLICANT: Wahl, Sharon M.
APPLICANT: Thompson, Robert C.
APPLICANT: Thompson, Robert C.
APPLICANT: Thompson, Robert C.
APPLICANT: Dripps, David J.
TITLE OF INVENTION: INHIBITION OF RETROVIRUS INFECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Elsenberg, Stephen
APPLICANT: Wahl, Sharon M.
APPLICANT: Wahl, Sharon M.
APPLICANT: Thompson, Robert C.
APPLICANT: Dripps, David J.
TITLE OF INVENTION: INHIBITION OF RETROVIRUS INFECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 2005-3315

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION TOPER: US/08/483,503A
FILING DATE: 07-JUN-1995
FILING APPLICATION NUMBER: US/08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION NUMBER: US/08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION NUMBER: US/07/943,369
FILING DATE: 09-SEP-1992
ATTOMENY/AGENT INFORMATION:
MANDEL ADDITED TO NUMBER: US/07/943,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04189.0084-02000
Sequence 3, Application US/08483503A Patent No. 6017880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08483503A Patent No. 6017880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET UMBER: 041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 44.69 hes 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECURING: 202-202 TELEPHONE: 202-400 TELEPHONE: 202-408-4400 TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-483-503A-3
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US-08-483-503A-4
                                                                                                                                                                                                                                                                                                                                                                         STATE:
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HYPOTHETICAL: FRAGMENT TYPE:
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Sequence 1, Application US/08304051

Patent No. 563327

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

INTILE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
41.3%; Score 135; DB 3; Length 107;
Best Local Similarity 44.6%; Pred. No. 8.9e-08;
Matches 25; Conservative 4; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,051
FILING DATE: 12-Sept-1994
CLASSIFICATION DATA: No. 5633227e
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
NAME: William F. Gray
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322
                                                                                                                                                                                                                       COMPOURE: IBM PC COMPATIBLE
COMPOURE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04189.0084-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,013
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-483-503A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Related to the sequence of the N-terminal domain of human SLPI. In the listed sequence Xaa at position 18 is Arg or Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise, Delaria,
APPLICANT: Matherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAYER Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.3%; Score 99; DB 1; Length 49; Best Local Similarity 38.6%; Pred. No. 0.00029; Matches 17; Conservative 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: System 7.1 SOFTWALE: Word Perfect 3.0a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SFKAGVCPKKSAQCXLRYKKPECQSDWQCPGKKRCCPDTCGIKC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 STKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURKENI APPLICATION DATA

CURKENI APPLICATION NUMBER: PCT/US95/11445

FILING DATE: 11 September 1995

CLASSIFICATION:
PRIOR APPLICATION ON:
PRIOR APPLICATION NUMBER: 08/304,051

PILING DATE: 12 SEPTEMBER 1994

ATTORNEY/AGENT INFORMATION:
NAME: William F. GRAY

REGISTRATION NUMBER: 31018

REGISTRATION NUMBER: 31018

REGISTRATION NUMBER: 31018

REFERENCE/DOCKET NUMBER: MWH 322PI

TELEPHONE: (203) 937-2712

TELEPHONE: (203) 937-5492

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       HYPOTHETICAL: Yes
FRAGMENT TYPE: N-terminal fragment
TELECOMMUNICATION INFORMATION:
                    TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-2795
TELEX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 amino acids
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                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                               LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                     - Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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GY: linear
                                                                                                                                                                    amino acid
GY: linear
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DESCRIPTION:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                               ), NAME/KEY;

), NAME/KEY:

US-08-304-051-1
                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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N-terminal fragment

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In the listed sequence Xaa at position
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                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James G
TITLE OF INVENTION: Polynucleotides and methods for their use.
FILE REPERBACE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
PRIOR APPLICATION NUMBER: US. No. 6380362 60/171,678
PRIOR PRILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 98; DB 4; Length 174;
33.8%; Pred. No. 0.0013;
Live 7; Mismatches 18; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EPVKGPVSTKP-----GSCPII----LIRCAMLNPPNRCLKDTDCPGIKKC 44
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APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Nurison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037c1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                     30.3%; Score 99; DB 5; Length 49; 38.6%; Pred. No. 0.00029; Live 5; Mismatches 22; Indels
                              the N-terminal
                                                                                                                                                                                                                            10 STKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                       4 SPKAGVCPKKSAQCXLRYKKPECQSDWQCPGKKRCCPDTCGIKC 47
                         Related to the sequence of domain of human SLPI. In t. 18 is Arg or Lys.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/09724864
Patent No. 6380362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09383586 Patent No. 6242419 GENERAL INFORMATION:
                                                                                                                                                           Local Similarity 38.69 tes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Conservative
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; FEATURE:
; NAME/KEY:
; NAME/KEY:
; NAME/KEY:
PCT-US95-11445-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                           US-09-724-864-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 56
                                                                                                                                          Query Match
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USE OF KAL PROTEIN AND TREATMENT WITH THE KAL PROTEIN IN TREATMENT OF RETINAL, RENAL, NEUROMAL AND NEURAL INJURY
                                                                                                                                                                                                                                                                                                                      APPLICANT:
TITLE OF INVENTION: NUCLEIC SEQUENCE OF THE GENE ASSOCIATED WITH
TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING
TITLE OF INVENTION: PEPTIDE SEQUENCES, DIAGNOSTIC APPLICATIONS.
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Gaps
                                                   17;
                                                                                             12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                       27 KPGACP-----KPSPESVGICVDQCSGDGSCPGNMKCCSNSCGHVCKTP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 28.3%; Score 92.5; DB 1; Length 680; Local Similarity 34.6%; Pred. No. 0.02; les 18; Conservative 3; Mismatches 20; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KPGSCPI-----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
28.9%; Score 94.5; DB 4; Length 72; 35.8%; Pred. No. 0.0013; ive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1758 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: PETIT, CHRISTINE
APPLICANT: SOUSSI-YAMITCOCTAS, NADIA
APPLICANT: SARAILH, CATHERINE
APPLICANT: ROUGON, GENEVIEVE
APPLICANT: ROUGON, GENEVIEVE
APPLICANT: LEGOUIS, RENAUD
APPLICANT: MAZIE, JEAN-CLAUDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08211430
; Patent No. 5763166
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08761136; Patent No. 6121231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OKGANISM: Homo sapiens
; CELL LINE: Foetal brain cell
US-08-211-430-2
                      Best Local Similarity 35.8
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                       US-08-211-430-2
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US-08-761-136-1
    Query Match
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17 PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFREATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: TURIEY, CHARLES P
REGISTRATION NUMBER: 35,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                Query Match 27.2%; Score 89; DB 2
Best Local Similarity 39.0%; Pred. No. 0.003
Matches 16; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 15
CORRESSONDENCE ADDRESS:
ADDRESSEE: Jenkens & Gilchrist
STRRET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
US-08-761-248B-13
US-08-761-248B-13
Sequence 13, Application US/08761248B
FATENT NO. 5958735
GENERAL INFORMATION:
APPLICANT: ROWLEY, DAVID R.
1TITLE OF INVENTION: UROGENITAL SINUS
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INPORMATION:
TELEPHONE: (713)9513310
TELEPHAX: (713)0513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 CLKDTDCPGIKKCCEGSCGMACFVPQ 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 13; Conservative
                                                    : 51 amino acids
amino acid
EDNESS: single
                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-08-761-248B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDAL.
STREET: LIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 77002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-761-248B-13
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US-09-152-060-75
                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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Sequence 14, Application US/08761248B
Patent No. 5958735
GENERAL INFORMATION:
APPLICANT: ROWLEY, DAVID R.
TITLE OF INVENTION: URGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 KQGDCPAPEKASGFAAACV----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
28.3%; Score 92.5; DB 3; Length 680;
Best Local Similarity 34.6%; Pred. No. 0.02;
Matches 18; Conservative 3; Mismatches 20; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 KPGSCPI----ILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
COUNTRY: ...
ZIP: 22202
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/761,136
FILING DATE: 06-DEC-1996
FILING DATE: ...
TANN: 435
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ZIP: 77002
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: U6-DEC-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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1100 Louisiana, Suite 1800
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REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 2,618
REFERENCE/DOCKET NUMBER: 660-
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-413-3000
TELEPHONE: 703-412-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-412-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (713)9513310
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REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: 110
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Gaps
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: UROGENITAL SINUS DERIVED GROWTH
: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
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Score 89; DB 2; Length ox, Pred. No. 0.0036;
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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Patent No. 5958735
GENERAL INFORMATION:
APPLICANT: ROWLEY, DAVID R.
TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLECTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 VOGPGLÍDWLFPRRCPKIREECE-FQERDVCTKDRQCQDNKKCCVFSCGKKC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.0%; Score 85; DB 4; Length 133; Best Local Similarity 40.4%; Pred. No. 0.025; Matches 21; Conservative 2; Mismatches 25; Indels
                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
Sequence 75, Application US/09152060 Patent No. 6448230 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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RESULT 28

US-08-761-248B-15

Sequence 15, Application US/08761248B

Sequence 15, Application US/08761248B

Sequence 15, Application US/08761248B

SETEM NO. 5958735

TITLE OF INVENTION: URGENITAL SINUS DERIVED GROWTH

TITLE OF INVENTION: PACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jenkens & Gilchrist

STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.8%; Score 84.5; DB 2; Length 44; Best Local Similarity 40.0%; Pred. No. 0.0094; Matches 14; Conservative 4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.5%; Score 83.5; DB 2; Length 42; 40.5%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761 2400
FILTRE NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 RCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QCLRYKKP-ECQSDWQCPGKKRCCPDTCGIKCLDP 41
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06-DEC-1996
NAME: Turiey, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TREECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTONEY/AGENT INFORMATION:
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 amino acids
                                                                                                TELEPHONE: (713)951331
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-761-248B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.99
Best Local Similarity 30.45
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (713)9513314
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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  Houston
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COUNTRY: USA
77002
                                     USA
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                                   COUNTRY:
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  Gaps
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APPLICANT: ROWLEY, DAVID R.
APPLICANT: ROWLEY, URGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLECTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jankens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ROWLEY, DAVID R.
TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: PACTOR NUCLECTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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  14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                         27 NPPNR-----CLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                            4 NPPRSIGTCVELCSGDQSCPNIQKCCSNGCGHVCKSP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTRACTOR SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08761248B
Patent No. 5958735
                                                                                                                                                                            Sequence 7, Application US/08761248B Patent No. 5958735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Turley, Charles P
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 Houston
                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-761-248B-7
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US-08-761-248B-2
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    15;
    Matches
                                                                                                                                          RESULT 29
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GENERAL INFORMATION:
APPLICANT: ROWLEY, DAVID R.
TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.9%; Score 81.5; DB 2; Length 212; 30.4%; Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PRTLPPGAC------QATRCQSDSECPRHRRCCYNGCAYAC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTOMNEY/AGENT INFORMATION:
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
                                                                                                                                                                                                                                                                                                      35,723
ER: 34012.6
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APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTONNEY,AGENT INFORMATION:
NAME: TUTIEY, Charles P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/08761248B
; Patent No. 5958735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08761248B
Patent NO. 5958735
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES NUMBER OF SEQUENCES:
ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                           Query Match
24.9%; Score 81.5; DB 2; Length 212;
Best Local Similarity 30.4%; Pred. No. 0.093;
Matches 14; Conservative 6; Mismatches 15; Indels 11
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24.3%; Score 79.5; DB 2; Length 220;
Best Local Similarity 30.4%; Pred. No. 0.16;
Matches 14; Conservative 6; Mismatches 15; Indels 11
                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          62 PRILPPGAC------QATRCQSDSECPRHRRCCYNGCAYAC 96
                                                                                                                                                                                                                                                                                                                                                                            8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC.1996
CLASSIFICATION: 435
    34012.6
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APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34(
TELECOMMUNICATION:
TELEPHONE: (713)9513310
                   TELECOMMUNICATION INFORMATION TELEPHONE: (713)9513310
                                                                                                    INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                             LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 amino acids
                                                               TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (713)951331
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston
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US-08-761-248B-4
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58 SAAGGSCRTPIIVPTPKAGRCPWVQAPMLSQLCEELSDCANDIECRGDKKCCFSRCAMRY 117
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33.3%; Pred. No. 0.13;
tive 4; Mismatches 22; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 STKPGSC--PIILI-----RCAMLNPP------NRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
70 PRTLPPGACQAA------RCQADSECPRHRRCCYNGCAYAC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/FF92/00533
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
APPLICATION NUMBER: FR 91/07179
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/162,146
FILING DATE: 10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09314127
Patent No. 6268545
GENERAL INFORMATION:
APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: THEPOT, Dominique
APPLICANT: THEPOT, Dominique
                                                                                                                                   ; Sequence 3, Application US/08162146; Patent No. 5965788; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.3%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-162-146-3
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
USA
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 LEP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 FVP 56
                                                                                                            US-08-162-146-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-09-314-127-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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RESULT 36
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Best Local Similarity 33.3%; Pred. No. 0.13;
Matches 21; Conservative 4; Mismatches 22; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 STKPGSC--PIILI-----RCAMENPP------NRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             % Sequence 12, Application US/08761248B

§ Sequence 12, Application US/08761248B

§ Patent No. 5958735

§ PATENT NO. 5958735

§ TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH

† TITLE OF INVENTION: PACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES

§ NUMBER OF SEQUENCES: 15

§ CORRESPONDENCE ADDRESS: 310RESSEE: Jenkens & Gilchrist

§ STREET: 1100 Louisiana, Suite 1800
TITLE OF INVENTION: Production of a Protein of Interest in TITLE OF INVENTION: the Milk of a Transgenic Mammalian NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,127
                                                                                  ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALL...
FILING DATE:
FILING DATE:
PROPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLd C.
REGISTRATION NUMBER: 25,258
TELEPHONE: (202) 672-5300
""" FFAX: (202) 672-5309
                                                                                                                                                           COMPUTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 127 amino acid TOPOLOGY: linear MOLECHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-314-127-3
                                                                                                   STREET: 3000 K SUCITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDAL
STREET: 112.
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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COUNTRY: US!
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Gaps
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; Sequence 21, Application US/08155171B
; Patent No. 5543264
; GENERAL INFORMATION:
    APPLICANT: Anderson, Carl W.
    APPLICANT: Mangel, Walter F.
    TITLE OF INVENTION: Co-Factor Activated Recombinant
    TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
    STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

20.5%; Score 67; DB 2; Length 44;
Best Local Similarity 30.4%; Pred. No. 0.7;
Matches 14; Conservative 5; Mismatches 15; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,171B
FILING DATE: 19-NOV-1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/851,217
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/851,217
FILING DATE: 29-JUN-1990
ATTORIEY/AGENT IMPORMATION:
AND ATTORIEY/AGENT IMPORTATION:
AND ATTORIEY/AGENT DATA:
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REFERENCE/DOCKET NUMBER: BNL91-01A2, AU193-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPRAX: (617) 861-9540
SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/761,248B
                                                                              APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION 1435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: TUTIEY, Charles P
REGISTRATION NUMBER: 35,723
REGISTRATION NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (713)951331
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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Gaps
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                                                                                                                                                  Query Match
19.1%; Score 62.5; DB 1; Length 202;
Best Local Similarity 34.3%; Pred. No. 9.6;
Matches 12; Conservative 10; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 62.5; DB 2; Length 202; 34.3%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08435998
Patent No. 5935840
GENERAL INFORMATION:
APPLICANT: Anderson, Carl W.
APPLICANT: Mangel, Walter F.
TITLE OF INVENTION: Co-Factor Activated Recombinant
TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                  92 LIKRSALSSPDKCVKVIKNSQSVQCTCAGSCGLFC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92. LIKRSALSSPDKCVKVIKNSQSVQCTCAGSCGLFC 126
                                                                                                                                                                                                                         20 LIRCAMINPPNRCLK-DTDCPGIKKCCEGSCGMAC 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                ; TOPOLOGY: linear
US-08-155-171B-21
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Matches 12; Conserv
                                                                          STRANDEDNESS:
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1101 SPKPGSPPL----CACLSGFGGPDCLTPPAPPGCGPPSPCLHNGTCTETPGL----GNP 1151
                                                                                 APPLICANT: Kitajewski, Jan
APPLICANT: Kitajewski, Jan
APPLICANT: Uyttendaele, Hendrik
TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
FILE REPERENCE: 53863-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/467,997
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                    19.1%; Score 62.5; DB 4; Length 1964;
29.9%; Pred. No. 91;
ive 7; Mismatches 11; Indels 29; Gaps
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TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: DOS
FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT: NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34012.6
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GENERAL INFORMATION:
GAPPLICANT: ROWLEY, DAVID R.
US-09-467-997-1
; Sequence 1, Application US/09467997
; Patent No. 6379925
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : (713)9513310
(713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
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SOFTWARE: FASTSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse
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                                                                                                                                                                                                                                                                                                   LENGTH: 1964
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38 amino acids

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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-491-976-3
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US-08-491-976-1
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                                                                                                                                                     Gaps
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Nathronia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                            Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%; Score 59; DB 4; Length 178; 27.9%; Pred. No. 20;
                                                                                                                                                 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGDRY INFORMATION:
NAME: Makk, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                          18.8%; Score 61.5; DB 2;
31.6%; Pred. No. 2.4;
trive 4; Mismatches 19;
                                                                                                                                                                                                                          1 CPELQ---ADONCTQECVSDSECADNLKCCSAGCATFC 35
                                                                                                                                                                                         16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       Sequence 297, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 297:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 178 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                Reed, Steven G.
                                                                                                                Query Match
Best Local Similarity 31.6%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
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             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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TOPOLOGY: linear
   amino acid
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
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                                                                 ; MULECULE 11F1
US-08-761-248B-11
                                                                                                                                                                                                                                                                                                       US-09-072-596-297
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RESULT 41

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ADDRESSEE: No. 57834160 No. 5783416disk of No. 5783416th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                       SSEE: No. 57834160 No. 5783416disk of No. 5783416th America, Inc.
F: 405 Lexington Avenue, 64th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.7%; Score 58; DB 1; Length 106; 36.2%; Pred. No. 15; tive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KPSPC----QCSRLSPHNR----TNCGFPGITSDQCFDNGC---CF 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bjorn, Soren E.
APPLICANT: Christensen, Mogens
APPLICANT: Nielsen, Per F.
TITLE OF INVENTION: Human Spasmolytic Polypeptide in
TITLE OF INVENTION: Glycosylated Form
                                                                      APPLICANT: Thim, Lars
APPLICANT: No. 5783416ris, Kjeld
APPLICANT: No. 5783416ris, Panny
APPLICANT: No. 5783416ris, Panny
APPLICANT: Bjorn, Soren E.
APPLICANT: Christensen, Mogens
APPLICANT: Nielsen, Per F.
TITLE OF INVENTION: Human Spasmolytic Polypeptide in
TITLE OF INVENTION: Glycosylated Form
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/491,976 FILING DATE: OZ-AUG-1995 CLASSIFICATION: 43-5 ATTORNEY/AGENT INFORMATION: NAME: Lamblris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thim, Lars
No. 5783416ris, Kjeld
No. 5783416ris, Fanny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/08491976
; Patent No. 5783416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3951.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
; Sequence 1, Application US/08491976; Patent No. 5783416; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.2
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: NO. 57834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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New York
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                                                                                                                                                                                      TOPOLOGY:
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US-08-896-449A-2
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                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SAITO, YASHUSHI
APPLICANT: IWASAKI, AKIO
APPLICANT: ARAI, YOLGHI
APPLICANT: YAMAZAKI, HIROYUKI
TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG PROTEIN AND
TITLE OF INVENTION: THE GENE CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.7%; Score 58; DB 1; Length 159; ilarity 36.2%; Pred. No. 23; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1752 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KPGSCPIILIRCAMLNPPNRCLKDTDC--PGI--KKCCEGSCGMACF 54
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/491,976
FILING DATE: 02-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGRAT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 3951.204-US
FELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,034
FILING DATE: 08-OCT-1996
PLIOR APPLICATION DATA:
APPLICATION NUMBER: UP 261440/1995
FILING DATE: 09-OCT-1995
PILING DATE: 09-OCT-1995
FILING DATE: 09-OCT-1996
FILING DATE: 24-APR-1996
FILING APPLICATION NUMBER: JP 102451/1996
FILING DATE: 24-APR-1996
ATTONENY/AGENT INFORMATION:
  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08727034
Patent No. 5665872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-976-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22202
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 43
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Gaps
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                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                     Query Match 17.7%; Score 58; DB 1; Length 2214; Best Local Similarity 35.4%; Pred. No. 3.1e+02; Matches 17; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.7%; Score 58; DB 3; Length 2813; Best Local Similarity 40.0%; Pred. No. 3.9e+02; Matches 18; Conservative 2; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1410 PFSTPGPSTCLPNYYRCS----SGTCVMDTWVCDGYRDCADGSDEEAC 1453
                                                                                                                                                                                                                                                                                                                                                                                                      8 PVSTK-PGSCPIILIRCAMLNPPNRCLKDT-DCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Venea, Patrick J
APPLICANT: Yuzbasiyan-Gurkan, Vilma
APPLICANT: Schall, William D
APPLICANT: Schall, William D
APPLICANT: Brewer, George J
TITLE OF INVENTION: PACTOR AND METHODS OF USE
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2199 CAMSCPPSLVYNHC--EHGCP---RLCEGNTSSCGDQPSEGCFCP 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 CAMLNPP----NRCLKDTDCPGIKKCCEG---SCG----MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,449A
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Harness, Dickey & Pierce, P.L.C.
5445 Corporate Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Smith, DeAnn F.
REFERENCE/DOCKET NUMBER: 2115-001226
TELECOMUNICATION INFORMATION:
TELEPHONE: 248-641-1600
TELEFAX: 248-641-0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/08896449A ; Patent No. 6040143
REFERENCE/DOCKET NUMBER: 8C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                  INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX. 287637
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2813 amino acids
                                                                                                                                                    LENGTH: 2214 amino acids
                                                                           703-413-2220
                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-727-034-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-896-449A-2
                                                                                                                                                                                amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Michigan
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STREET: 5.
Troy
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                                                                                                      APPLICANT: Variation Farrick J
APPLICANT: Variation Farrick J
APPLICANT: Varbasiyan-Gurkan, Vilma
APPLICANT: Varbasiyan-Gurkan, Vilma
APPLICANT: Stewer, George J
APPLICANT: Brewer, George J
APPLICANT: Duffendeck, John
TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
TITLE OF INVENTION: OF USE
TITLE REFERENCE: 2115S-001226CPB
CURRENT PAPLICATION NUMBER: US/09/132,652
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/896,449
EARLIER APPLICATION NUMBER: 08/896,449
EARLIER PILING DATE: 1999-07-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DIA
CONTAINING THE GENE ENCOING LOW DENSITY LIPOPROTEIN RECEPTOR
CONTAINING THE GENE ENCOING LOW DENSITY LIPOPROTEIN RECEPTOR
HUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/396,697
FILING DATE: 22-AuG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 313,682
FILING DATE: 22-FBE1989
FILING DATE: 22-FBE1989
FILING DATE: 23-AuG-1988
FILING DATE: 23-AuG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.6%; Score 57.5; DB 6; Length 726; Best Local Similarity 34.1%; Pred. No. 1.2e+02; Matches 14; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.7%; Score 58; DB 3; Length 281
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2199 CAMSCPPSLVYNHC--EHGCP---RLCEGNTSSCGDQPSEGCFCP 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 CAMLNPP----NRCLKDTDCPGIKKCCEG---SCG----MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 GTCQPTQFRC----PDHRCISPLYVCDGDKDCADGSDEAGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GSCPIILIRCAMLNPPNRCLKDT-DCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08785530 Patent No. 5814480 GENERAL INFORMATION:
                          Sequence 2, Application US/09132652
Patent No. 6074832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5208144-37
;Patent No. 5208144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 2813
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US-08-785-530-3
US-09-132-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-132-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;SEQ ID NO:37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5208144-37
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.3%; Score 56.5; DB 2; Length 6
Best Local Similarity 34.1%; Pred. No. 13;
Matches 15; Conservative 2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 Tredsc----AcA-----GSCKCKECKCTSCKKCCSCCPVGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 TKPGSCPIILIRCAMLNPPNRC-LKDTDCPGIKKCCEGSCGMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDS COMPATIONE
COMPUTER: DISKETTE DOS
SOFTWARE: FASTERO for Windows Version 2.0
CURRENY APPLICATION DATA:
FILING DATE:
                                                                                                COMPUTER READBLE FORM:
MIDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERE FOR Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0194 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,530
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09123850
; Patent No. 5955428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
        3174 Porter Drive
                                                                                                                                                                                                                                      FILING DATE: Herewith CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
STREET: 31/7 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenB
CLONE: 386962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
                                                                                    94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Pal
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-123-850-3
                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-785-530-3
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1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Janice
                                                                                       78 ONPODESPDISPPICERKTASFGYLDRSPSACKRDIQKESVQGAAQDVAGVAACLP 133
                                                 2 QEPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                   APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Levas, Ullian H.
APPLICANT: Levas, Ullian H.
APPLICANT: Pleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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GENERAL INFORMATION:
APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Ja
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.3%; Score 56.5; DB 3; Length 1257; Best Local Similarity 32.4%; Pred. No. 2.66+02; Matches 12; Conservative 6; Mismatches 14; Indels 5;
       32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLILOMEDR: US/08/611,729A
FILING DATE: 06-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             963 PIRNPIE-RPGGHKDVLYQCKNFTPPPR----RRCPG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPG 40
       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7326-037
                                                                                                                                                                                                      ; Sequence 8, Application US/08611729A; Patent No. 6004924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/08390882A
; Patent No. 5688764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1257 amino acids
    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-611-729A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                           RESULT 50
US-08-611-729A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-08-390-882A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches 16; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lichy, Jack H
APPLICANT: Lichy, Jack H
APPLICANT: Lichy, Deter M
TITLE OF INVENTION: HTSI-Gene, A Human Tumor Suppressor Gene
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend
STREET: I Market plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56.5; DB 1; Length 1137; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%; Score 56.5; DB 2; Length 61; 34.1%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 TKPGSCPIILIRCAMLNPPNRC-LKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TTGGSC----ACA----GSCKCKECKCTSCKKCCCSCCPVGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                  PF-0194 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/916,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15280-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-369-043-2; Sequence 2, Application US/08369043; Patent No. 5491064; GENERAL INFORMATION:
                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.3%;
25.0%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1137 amino acids
                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                       GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Loçal Similarity
                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBac
CLONE: 386962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                US-09-123-850-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-369-043-2
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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RESULT 49

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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-390-882A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
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Patent No. 5688764

GENERAL INFORMATION:
APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Ja
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
STREET: 170 SOUTH MAIN STREET
CITY
CORRESPONDENCE METCALF
STREET: 170 SOUTH MAIN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.1%; Score 56; DB 1; Length 39; Best Local Similarity 45.0%; Pred. No. 9.4; Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM
  ADDRESSEE: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
STREET: 170 SOUTH MAIN STREET
CITY: SALT LAKE CITY
                                                                                                                                                                                                                               OCHERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,882A
FILING DATE: No. 5688764e assigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFERENCE/DOCKET NUMBER: 1094.2.1
TELECOMMUNICATION INFORMATION:
TELEPRAX: (801) 537-1700
TELEPRAX: (801) 537-1700
TELEPRAX: (801) 537-1700
TELEPRAX: (801) 537-1700
TELEPRAX: (801) 537-1700
TELEPRAX: (801) 537-1700
TELEROMETION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,882A
FILING DATE: No. 5688764e assigned
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Calisoga sp. INDIVIDUAL ISOLATE: peptide B ORGANELLE: Venom glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CPGIKKCCEGSCG--MACFV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CSNSKDCCSGNCGTFWTCFI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                             STATE: UTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 84101
                                                                                                                                            84101
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US-08-390-882A-3
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                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: STATE:
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Gaps
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Sequence 6, Application US/08911423

Sequence 6, Application US/08911423

Patent No. 6111090

GENERAL INFORMATION:

APPLICANT: Randall, Troy D.

APPLICANT: ALlotnik, Albert

TITLE OF INVENTION: RAMMALIAN CELL SURFACE ANTIGENS; RELATED

TITLE OF INVENTION: REAGENTS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET 901 California Avenue

CITT: Palo Alto

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.1%; Score 56; DB 1; Length 39;
Best Local Similarity 45.0%; Pred. No. 9.4;
Matches 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALITORINA
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APERICALION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-NG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-07-07-07
APPLICATION NUMBER: US 60/027,901
FILING DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-07-07-07
NAME: Ching, Edwin P.
RESISTRATION NUMBER: 34,090
FRIENTATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Calisoga sp.
INDIVIDUAL ISOLATE: peptide C
ORGANELLE: Venom glands
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFRENCE/DOCKET NUMBER: 1094
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 537-1709
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISITICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 CPGIKKCCEGSCGM--ACFV 55
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                                                                                                                                                                                                                                                                single
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MOLECULE TYPE: peptide
HYPOTHETICAL:
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2 QEPVKGP------VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                          20 QRPTGGPGCPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77
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25.8%; Pred. No. 57;
ktive 4; Mismatches 30; Indels 12; Gaps
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                                                                                                                                                                                                                                                                  Sequence 4, Application US/08911423
Patent No. 611090
Patent No. 611090
PAPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS, RELATED TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES. 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION: TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
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amino acid
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Best Local Similarity 25.8%
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-911-423-4
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California
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STREET: 90
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US-08-911-423-4
                                                                                                                  52 AC 53
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                                                                                                                                                         78 PC 79
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US-08-937-931-6
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                                                                                                                                                                     Query Match 17.1%; Score 56; DB 3; Length 228; Best Local Similarity 25.8%; Pred. No. 54; Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps
                                                                                                                                                                                                                                                           2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                 20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-911-423-7
Sequence 7, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAWMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%; Score 56; DB 3; Length 232; 25.8%; Pred. No. 55; tive 4; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-4NG-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-4NG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
RAPPLICATION NUMBER: US 60/027,901
RILING APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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Matches, 16; Conservative
                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-911-423-6
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ADDRESSE: DNAX Rese
STREET: 901 Californ
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California
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CORRESPONDENCE ADDRESS: CORRESPECS: SCIENCE & TECHNOLOGY LAW GROUP STREET: SCIENCE & TECHNOLOGY LAW GROUP CITY: SAN FRANCISCO CITY: SAN FRANCISCO STATE: CALIFORNIA
Sequence 6, Application US/08937931
Patent No. 5935792
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
APPLICANT: Pan, Duojia
APPLICANT: Rooke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KIZ: A No. 5935792el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
APPLICANT: AND APPLICANT: AND APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 
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17.1%; Score 56; DB 2; Length 265;
11 Similarity 28.6%; Pred. No. 62;
18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,931
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSHAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
ITELEFACE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
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Patent No. 6190876
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
APPLICANT: Rook, Jenny
APPLICANT: Rook, Jenny
APPLICANT: Xavari, Reza
APPLICANT: Xavari, Reza
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-285-502-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-937-931-6
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Rooke, Jenny
Yavari, Reza
Xu, Tian
TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 4; Length 265; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SCIENCE & TECHNOLOGY LAW
CITY: SAN FRANCISCO
STATE: CALIFORNIA
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/285,502
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-No. 6319704-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,502
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                    APPLICATE...

FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09709126
Patent No. 6319704
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.1%;
Best Local Similarity 28.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan, Duojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-09-285-502-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 FVP 56
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US-09-871-385A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 60
US-08-911-423-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, Tian TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AREGICNGFTA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AQEPVKGPVSTKPG-SC----PIILIRCAMINPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,385A
FILING DATE: 31-May-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                   NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-No. 6399350-2000
APPLICATION NUMBER: 09/285,502
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: OSMAN, RICHARD A
REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                     TYPE: amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-709-126-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09871385A
Patent No. 6399350
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
Pan, Duojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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Yavari, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 56; DB 4; Length 265; 28.6%; Pred. No. 62; tive 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%; Score 56; DB 3; Length 311; 25.8%; Pred. No. 73; ative 4; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-196
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: US 60/027,901
FILING DATE: 07-OCT-196
ATOMES, GATOMER: US 60/027,901
FILING DATE: 07-OCT-196
ATOMES, GATOMER: 34,090
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 amino acids
                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-911-423-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity '
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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RESULT 61
US-09-030-335-2

Sequence 2, Application US/09030335

Factorice 2, Application US/09030335

APPLICANT: Tindal, Michael H

APPLICANT: Hagqi, Tariq M

TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,

TITLE OF INVENTION: Fragments and the Like

TITLE OF INVENTION: Fragments and the Like

TITLE OF INVENTION: Where: US/09/030,335

CURRENT APPLICATION NUMBER: US/09/030,335

CURRENT PELLING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 2

LENGTH: 491

TYPE: PRT

ORGANISM: Homo sapiens

US-09-030-335-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AREGICNGFTA 284
                                 20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGBECCSEWDCMCVQP--EFHCGD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08920234
; Patent No. 5922546
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN DISINIFERIN METALLOPROTEASE
; TITLE OF INVENTION: HUMAN DISINIFERIN METALLOPROTEASE
; TITLE OF INVENTION: HUMAN DISINIFERIN METALLOPROTEASE
; TITLE OF INVENTION: RELATED TO DROSOPHILA KUZ GENE
; WUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAINER & PRESTIA
; STREET: PO. BOX 980
; CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,234
FILING DATE: 25-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.1%; Score 56; DB 4; I
Best Local Similarity 28.6%; Pred. No. 1.1e+02;
Matches 18; Conservative 5; Mismatches 28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
  2 QEPVKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 LCP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 FVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-920-234-2
                                                                                                 52 AC 53
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APPLICANT: Rubin, Gerald M.
APPLICANT: Roke, Jenny
APPLICANT: Pan, Ducjia
APPLICANT: Roke, Jenny
APPLICANT: Yavazi, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                          Query Match 17.1%; Score 56; DB 2; Length 748; Best Local Similarity 28.6%; Pred. No. 1.7e+02; Matches 18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SCIENCE & TECHNOLOGY LAW GROUP 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 997-081
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 343-4341
TELEPRAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amina acids
                                                  GH-70237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08937931
Patent No. 5935792
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: GH-7/
TELECOMMUNICATION INFORMATION:
TELEPAX: 610-407-0701
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                              STRANDEDNESS: single;
TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-920-234-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear / MOLECULE TYPE: peptide US-08-937-931-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 268 BUSH STR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 LCP 544
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US-08-937-931-4
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4;
                                                                                                        12; Gaps
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APPLICANT: Yavari, Reza
APPLICANT: Yavari, Reza
APPLICANT: Yu, Tian
TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AREGICNGFTA 541
                                                                               1 AQEPVKGPVSTKPG-SC----PILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
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Query Match
17.1%; Score 56; DB 2; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 258 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B97-081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/937,931 FILING DATE:
                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09285502
Patent No. 6190876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 89.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, Duojia
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 18; Conserve
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                                                                                                                                                                                                                                                             RESULT 64
US-09-285-502-4
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APPLICANT: Tindal, Michael H
APPLICANT: Tindal, Michael H
APPLICANT: Haggi, Tarig M
APPLICANT: Haggi, Tarig M
TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
TITLE OF INVENTION: Fragments and the Like
FILE REFERENCE: Metalloprotease
CURRENT APPLICATION NUMBER: US/09/030,335
CURRENT APPLICATION NUMBER: US/09/030,335
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
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CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 56; DB 4; 1
28.6%; Pred. No. 1.7e+02;
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APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-No. 6319704-2000
CLASSIFICATION: <a href="https://www.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.numbe
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/285,502
FILING DATE: <Unknown>
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REGISTRATION NUMBER: 36,627
                                  ; Sequence 9, Application US/09030335; Patent No. 6255064; GENERAL INFORMATION:
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Patent No. 6319704
GENERAL INFORMATION:
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TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
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Pan, Duojia
Rooke, Jenny
Yavari, Reza
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-030-335-9
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SEQUENCE CHARACTERISTICS:

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PATENT NO. 353.724
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
APPLICANT: Rooke, Jenny
APPLICANT: Rooke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INFORMATION: KUZ: A No. 5935792el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                     488 ANQPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AKEGICNGFTA 542
    Gaps
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                                            1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
    12;
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    28; Indels
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APPLICATION NUMBER: US/08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%; Score 56; DB 2;
28.6%; Pred. No. 1.7e+02;
live 5; Mismatches 28
    5; Mismatches
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 897-081
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                   RESULT 68
US-08-937-931-8
; Sequence 8, Application US/08937931
; Patent No. 5935792
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; Sequence 8, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 28.6
Matches 18; Conservative
    18; Conservative
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94104
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                                                                                                                                 54 FVP 56
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    Matches
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                                                                                                                                                                                                                   4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu, Tian
TITLE OF INVENTION KUZ: A No. 6399350el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                 487 ANOPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AREGICNGFTA 541
                                                                                                                                                                                                                                                         1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%; Score 56; DB 4; Length 748; 28.6%; Pred. No. 1.7e+02;
                                                                                                                                                                         Length 748;
                                                                                                                                                                                                                   28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                         Score 56; DB 4;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-00. 6399350-2000
APPLICATION NUMBER: 09/285,502
FILING DATE: «Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INPORMATION:
TELECHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/871,385A
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                  MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09871385A Patent No. 6399350 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
LENGTH: 748 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rubin, Gerald M. Pan, Duojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                   STRANDEDNESS: single
                                                                                                                                                                       Query Match
Best Local Similarity 28.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rooke, Jenny
Yavari, Reza
                                                                roPoLoGY: linear
                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        542 LCP 544
                                                                                                                                                                                                                                                                                                                                           54 FVP 56
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                                                                                                                               US-09-709-126-4
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54 FVP 56
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TITLE OF INVENTION: KUZ: A NO. 6319704el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
                                                     APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 ANOPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AKEGICNGFTA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY. STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,502
                                                                                                                                                         ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Policial
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTATION UNMBER: 36,627
REPERENCE/DOCKET NUMBER: 897-0
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09709126
Patent No. 6319704
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rubin, Gerald M.
Rubin, Gerald M.
Pan, Duojia
Rooke, Jenny
Yavari, Reza
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Yavari, Reza
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                                                                                                                                                                                                                       USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy A:
COMPUTER: IRM COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 LCP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 FVP 56
  APPLICANT:
                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-285-502-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
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Xu, Tian
TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 ANQPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AKEGICNGFTA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
17.1%; Score 56; DB 4; Length 749;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,126
FILING DATE: 08 No. 6319704-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN PRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/871,385A
FILING DATE: 31-May-2001
CLASSIFICATION: <URKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/709,126
                                                                                                                                                                                                                                                                                                                                              NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/285,502
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/09871385A
; Patent No. 6399350
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 749 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rubin, Gerald M.
Pan, Duojia
Rooke, Jenny
Yavari, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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AN ISOLATED POLYPEPTIDE RELATED TO THE EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND BIOASSAYS AND METHODS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 SCPHNFVVDQTSCVRACPPDK -- MEVDKNGLKMCEPCGGLCPKAC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SCP----ILLIRCAMINPPNRCLKDTDCPGIKKC--CEGSCGMAC 53
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COMPUTER: ISM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                      COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/978,895
FILING DATE: 19921110
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414-028
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1969
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Plowman, Gregory D. APPLICANT: Culouscou, Jean-Michel APPLICANT: Shoyab, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08484438; Patent No. 5811098; Patent No. 5811098 5780031
                                                                                                                                             STREET: 133 Carnegie Way, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1342 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                           Suite 400
                                                                                                   CORRESPONDENCE ADDRESS:
                                                                              NUMBER OF SEQUENCES:
         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
: U.S.A.
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                                                                                                                                                                                             Georgia
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                   Atlanta
                                                                                                                                                                                                                                          30303
                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                      STATE: Ge
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-484-438-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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APPLICANT: Tindal, Michael H
APPLICANT: Hadgi, Tariq M
TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
TITLE OF INVENTION: Exagments and the Like
FILE REFERENCE: Metalloprotease
CURRENT APPLICATION NUMBER: US/09/030,335
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 ANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDC----AREGICNGFTA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AQEPVKGPVSTKPG-SC----PIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSC-GMAC 53
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17.1%; Score 56; DB 4; Length 799;
Best Local Similarity 28.6%; Pred. No. 1.9e+02;
Matches 18; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.1%; Score 56; DB 4; Length 749;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels
              FILING DATE: 08-No. 6399350-2000 APPLICATION NUMBER: 09/285,502
                                                                                                   NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07978895
Patent No. 5480968
GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
                                                                                                                                                                                                                                                                                  LENGTH: 749 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-030-335-4; Sequence 4, Application US/09030335; Patent No. 6255064
                                                                                                                                                                                                                    343-4342
                                                           FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aaronson, Stuart A
                                                                                                                                                                                                                TELEFAX: (415) 343-4
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 799
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09-833799-13b.rai

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Matches
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Patent No. 5820859
GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: BIDASSAYS AND METHODS RELATED THERETO, AND
TITLE OF INVENTION: BIDASSAYS AND METHODS RELATED THERETO
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 400
STREET: ALS CATHEGIE Way, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 SCPHNFVVDQTSCVRACPPDK--MEVDKNGLKMCEPCGGLCPKAC 331
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CLEASITION DATA:
APPLICATION NUMBER: US/08/473,119
RILNG DATE: 07-JUN-1995
APPLICATION NUMBER: 07/978,895
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1989
ATTOPNEY/AGENT INFORMATION:
                                              PETING NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/23,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION S30
PRIOR APPLICATION S30
PRIOR APPLICATION UNMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-438-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 133 carred CITY: Atlanta STATE: Georgia
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ZIP: 30303
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US-08-473-119-4
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8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SCP----IILIRCAMLNPPNRCLKDTDCPGIKKC--CEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 11, 2003, 08:37:58 Job time: 20 secs
NAME: PERIYMAN, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414-028
TELEPHONE: (404) 688-0770
TELEPHONE: (404) 688-0770
TELEPHONE: CHAPACTERISTICS:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-473-119-4
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence

Sequence

Sequence

Sequence

Sequence

Sequence

Sequence Sequence

Sequence 59, Appl Sequence 58, Appl Sequence 38, Appl Sequence 42, Appl Sequence 42, Appl Sequence 136, Appl Sequence 136, Appl Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl

119, App 120, App 241, App 250, App 2, Appli 34921, A

Sequence Sequence Sequence

Sequence 350 Sequence 333,

Sequence

Sequence 4

Sequence

Sequence Sequence

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Sequence

Sequence

Sequence

Sequence 120, Sequence 241,

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US-09-749-837A-333

US-09-894-882-476

US-09-894-882-462

US-09-894-882-462

US-09-894-882-488

US-09-894-882-488

US-09-894-882-262

US-09-894-882-262

US-09-894-882-262

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US-09-894-882-262

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US-09-788-626-5264

US-09-894-882-356

US-09-915-593-28

US-09-915-593-28

US-09-915-593-28

US-09-915-593-28
US-09-90-21A-127
US-09-90-853-127
US-09-907-81-127
US-09-904-011-127
US-09-904-011-127
US-09-906-742-312
US-01-028-072-312
US-10-121-049-312
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19.7
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56.53
   February 11, 2003, 08:37:41; Search time 97 Seconds (without alignments) 15.013 Million cell updates/sec
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Sequence 345,
Sequence 345,
Sequence 345,
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Sequence 345,
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Sequence 345,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence
Sequence
                                                                                                                                   1 aqepvkgpvstkpgscpiil......cpgikkccegscgmacfvpq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                              CGRIZ_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

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(GGRZ_6/ptodata/2/pubpaa/NGO7_PUBCOMB.pep:*

(GGRZ_6/ptodata/2/pubpaa/NGO7_PUBCOMB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

(GGRZ_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

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(GGRZ_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-790-264-61
US-09-965-812-2
US-09-992-598-345
US-09-999-735-345
US-09-999-736-345
US-09-999-736-345
US-09-991-181-345
US-09-991-181-345
US-09-991-34-345
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US-09-991-34-345
US-09-991-34-345
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                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      140259 segs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                       Applications AA:*
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                               09-833799-13B
                                                                                                                                                                                                                                                                                                       Published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.3
34.3
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                                                                                                              Title:
Perfect score:
                                                                                                                                                        Scoring table:
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                                                                                                                                    Sequence:
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                                                                      Run on:
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253, App 262, App 265, App 477, App 286, App 353, App 97, App 242, App 242, App 242, App

Sequence 3 Sequence 3 Sequence 9 Sequence 2 Sequence 2

Sequence

Sequence 251, Applisequence 1, Applisequence 10742, A Sequence 2, Applisequence 472, Applisequence 2, Applisequence 271, Applisequence 271, Applisequence 274, Applisequence 478, Applisequence 478, Applisequence 38020, A Sequence 356, Applise

, Appl Appli Appli

Sequence

Sequence 127, P Sequence 127, P Sequence 127, P

Sequence 6,

Result

Sequence

Sequence 127, Sequence 127,

Sequence 312, Sequence 312, Sequence 127,

Gaps

0;

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APPLICANT: Ratelli, Luca
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Method of Detecting inflammatory Lung Disorders
FILE REFRENCE: 21402-018 US
CURRENT APPLICATION NUMBER: US/09/865,812
CURRENT FILING DATE: 2001-05-28
PRIOR PPLICATION NUMBER: 60/207,104
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                               78 PIRKPVWRKPGRCVKTQARCMMLNPPNVCQRDGQCDGKYKCCEGICGKVCLPP 130
                                                                                                                                                                                                                         4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                         49.2%; Score 161; DB 10; Length 131; 52.8%; Pred. No. 2.8e-09; tive 3; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
43.7%; Score 143; DB 10; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.6e-07;
Matches 27; Conservative 4; Mismatches 23; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 61 LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 345, Application US/09992598
; Patent No. US20020160384A1
                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-865-812-2
; Sequence 2, Application US/09865812
; Patent No. US20020115626A1
; GENERAL INFORMATION:
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Gurney, Austin L.
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Williams, P. Mickey
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Stewart, Timothy A.
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Gerritsen, Mary E.
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                                                                                                                                                                                       28; Conservative
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Botstein, David
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ORGANISM: Homo sapiens
                                                                                    ORGANISM: Mus musculus
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                                                                                                                                                                  Sest Local Similarity
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Patent No. US2002028508A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
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Fatent No. US20020052468A1
GENERAL INFORMATION:
APPLICANT: CONKIIN, Darrell
TITLE OF INVENTION: Disulfide Core Polypeptides
FILE REFERENCE: 99-1301
CURRENT FFLIANG DATE: 2001-01-0
PRIOR APPLICATION NUMBER: US/09/757,908A
PRIOR APPLICATION NUMBER: US 09/326,039
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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    US-10-123-904-312
US-10-140-470-312
US-09-906-838-127
US-09-907-613-127
US-09-907-942-127
US-10-175-918-312
US-10-176-918-312
US-10-176-921-312
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TILLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
PRIOR PEPLICATION NUMBER: US 09/065,661
PRIOR PELING DATE: 1998-04-23
PRIOR PELING DATE: 1998-04-23
PRIOR PELING DATE: 1998-04-23
PRIOR PILING DATE: 1998-06-23
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US-09-757-908A-7
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APPLICATION NUMBER: 60/090690
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                         APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                          PRIOR PELING DATE: J097-06-16
PRIOR PLILING DATE: J097-06-16
PRIOR PLILING DATE: J097-06-16
PRIOR PELING DATE: J097-06-17
PRIOR PELING DATE: J097-06-17
PRIOR PELING DATE: J097-01-17
PRIOR PELING DATE: J097-11-12
PRIOR PELING DATE: J097-11-13
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PRIOR PELING DATE: J097-11-13
PRIOR PELING DATE: J097-11-24
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Wood, William I.
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R FILING DATE: 1998-06 11

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R APPLICATION NUMBER: 60/088861

R APPLICATION NUMBER: 60/089105

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R FILING DATE: 1998-06-12

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R FILING DATE: 1998-06-16

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R FILING DATE: 1998-06-16 R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-16 1998-06-19 1998-06-17 FILING DATE: 1998-06-22 1998-06-17 FILING DATE: 1998-06-22 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: FILING DATE: FILING DATE:

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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            PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
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Sequence 345, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni,Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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FILING DATE: 1998-06-25
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Napier, Mary A.
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/065110
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PLING DATE: 1998-10-25
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APPLICATION NUMBER: 60/049787
FILING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
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IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
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                                                                                                           R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091548
R ALLING DATE: 1998-07-01
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091633
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
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. Sequence 345. Application US/09989735
. Publication No. US2020193299A1
. GENERAL INFORMATION:
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/090862
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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Goddard, Audrey
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Gerber, Hanspeter
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088202
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16 LLING DATE: 1998-06-04 PPLICATION NUMBER: 60/088326 LLING DATE: 1998-06-04 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 ICATION NUMBER: 60/088030 NG DATE: 1998-06-04 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089105 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 FILING DATE: 1938-02-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088028 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/087609 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-04 FILING DATE: 1998-06-03 FILING DATE: 1998-06-12 1998-05-07 1998-06-02 1998-06-02 FILING DATE: 1998-06-1 LING DATE: FILING DATE: LING DATE: FILING DATE: PRILOR
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PRIOR APPLICATION NUMBER: 60/08532
PRIOR FILING DATE: 1998-06-17
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                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                           5
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42.9%; Pred. No. 0.00014;
tive 6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                       24; Indels
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CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR PELICATION NUMBER: 60/06250

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/06570

PRIOR APPLICATION NUMBER: 60/06770

PRIOR APPLICATION NUMBER: 60/06770

PRIOR APPLICATION NUMBER: 60/06770

PRIOR APPLICATION NUMBER: 60/06571

PRIOR APPLICATION NUMBER: 60/06770

PRIOR APPLICATION NUMBER: 60/075945

PRIOR PILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-20
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091544
DR FILING DATE: 1998-07-01
DR FILING DATE: 1998-07-01
DR FILING DATE: 1998-07-02
DR FILING DATE: 1998-07-02
DR FILING DATE: 1998-07-02
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091633
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
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DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Ferrara, Napoleone
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Goddard, Audrey
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Best Local Similarity 42.99
Matches 24; Conservative
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Botstein, David
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R FILING DATE: 1998-04-28

R APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/087106

R FILING DATE: 1998-05-28

R APPLICATION NUMBER: 60/087607

R PILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/087609

R APPLICATION NUMBER: 60/087609
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R FILING DATE: 1998-06-03
A PAPLICATION NUMBER: 60/088021
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/086033

R APPLICATION NUMBER: 60/086326

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/08861
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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APPLICATION UNMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/091633

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R APPLICATION NUMBER: 60/090535
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090540
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-27
R APPLICATION NUMBER: 60/090557
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
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R APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090349
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R APPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090431
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                                FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
                                                                FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-01-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-10-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
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PRIOR PELING DATE: 1998-05-28
PRIOR PELING DATE: 1998-05-28
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PRIOR PELING DATE: 1998-05-28
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION WUMBER: 60/091978
PRIOR PAPLICATION WUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR PLING DATE: 1998-07-09
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Gurney,Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Eaton, Dan L.
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Matches 24;
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US-09-989-730-345
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R FILING DATE: 1998-06-02

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R FILING DATE: 1998-06-04 R FLING DATE: 1998-06-05
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R FILING DATE: 1998-06-17

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R APPLICATION NUMBER: 60/089598

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APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC14
CURRENT PAPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 1997-06-16
FRIOR APPLICATION NUMBER: 60/06250
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                                                                                                                                                                                                                      20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
                                                   34.3%; Score 112; DB 9; Length 111; 42.9%; Pred. No. 0.00014; ative 6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 345, Application US/09990436 Publication No. US20020198148A1 GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Botstein, David
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                                                          Query Match
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34.3%; Score 112; DB 9; Length 111; larity 42.9%; Pred. No. 0.00014; Conservative 6; Mismatches 24; Indels
PRIOR FILING DATE: 1998-06-19
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C53
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CURRENT FILING DATE: 2001-11-16
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                        Sequence 345, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
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Goddard, Audrey
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Eaton, Dan L.
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US-09-991-181-345
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PRIOR APPLICATION NUMBER: 60/088028

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730HORS: US/09/993,687
CURRENT APPLICATION NUMBER: US/09/993,687
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R APPLICATION NUMBER: 60/065186
R PILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
R APPLICATION NUMBER: 60/066770
R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088025
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FILLING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
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Grimaldi, J.Christopher
Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Goddard, Audrey
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R APPLICATION NUMBER: 60/088202 R FILING DATE: 1998-06-05 R APPLICATION NUMBER: 60/088212 R FILING DATE: 1998-06-05 R APPLICATION NUMBER: 60/088217 R PILING DATE: 1998-06-05 APPLICATION NUMBER: 60/08940 FILING DATE: 1998-06-12 FILING DATE: 1998-06-1 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
LING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
APLICATION NUMBER: 60/090429
APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/08824 60/088858 CATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089514 60/089532 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090254 1998-06-05 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/ 1998-06-09 1998-06-16 1998-06-17 FILING DATE: 1998-06-19 FILING DATE: 1998-06-19 1998-06-22 1998-06-22

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC64
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CURRENT PILLING DATE: 2001-11-19
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PRIOR FILLING DATE: 1997-06-16
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6; Mismatches 24,
                                                                               PRIOR APPLICATION NUMBER: 60/09044
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090412
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                        APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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Matches 24; Conserv
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Sequence 345, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Desteah, David
APPLICANT: Besteah, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.

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# FILING DATE: 1998-06-05

# APPLICATION NUMBER: 60/08855

# PILING DATE: 1998-06-09

# APPLICATION NUMBER: 60/088734

# FILING DATE: 1998-06-10

# PELLING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-16
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PILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
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APPLICATION UNWBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/
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R APPLICATION NUMBER: 60/090542
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-25
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Publication No. US20030008297A1
GENERAL INFORMATION:
                                                 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/091982
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Goddard, Audrey
Godowski, Paul J.
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Gerber, Hanspeter
                    1998-06-2
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Botstein, David
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US-09-997-653-345
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Gaps

Grimaldi, J. Christopher

APPLICANT:

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APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TITIES OF INVERTION: Socreed and Transmembrane Polypeptides and Nucleic TITIES OF INVERTION: Socreed and Transmembrane Polypeptides and Nucleic CIRRER REPRENCE: P273047, 2631

CURRENT PAPLICANTON: Acids Encoding the Same CIRRER REPRENCE: P27301211. 2997. 6531

CURRENT PAPLICANTON: Acids Encoding the Same PRIOR PAPLICANTON NUMBER: 6/06250

PRIOR PLING DATE: 1997-11. 2997. 6531

PRIOR PLILING DATE: 1997-11. 2997. 11. 2997. 11. 2997. 11. 2997. 11. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 2997. 299
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
                                                                                                                                                                                                                             Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                          Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                         Pan, James
Paoni, Nicholas F.
Gurney, Austin L.
                              Kljavin, Ivar J.
Napier, Mary A.
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/088138
PRIOR FILING DATE: 1998-06-10
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                            FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                               CURRENT AFFLIAND NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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Williams, P. Mickey
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R APPLICATION NUMBER: 60/090696
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Publication No. US20030022187A1
GENERAL INFORMATION:
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-06-24
APPLICATION WINBER: 60/090542
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APPLICATION NUMBER: 60/092182
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FILING DATE: 1998-06-25
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FILING DATE: 1998-07-02
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Gurney, Austin L.
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Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                 PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
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PRIOR APPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090862
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PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
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; Sequence 345, Application US/09990438
; Publication No. US20030027754A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/092182
APPLICATION NUMBER: 60/090678
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Watanabe, Colin K.
Williams, P. Mickey
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Roy, Margaret Ann
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Gerber, Hanspeter
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Eaton, Dan L.
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THIE REFERENCE: P2730PLC3
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PRIOR PADLICATION NUMBER: 05/049797
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PRIOR PADLICATION NUMBER: 06/065186
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CURRENT APPLICATION NUMBER: US/09/990,562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                                                             PRIOR FILING DATE: 1998-06-26
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DR APPLICATION NUMBER: 60/091478
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PRIOR FILING DATE: 1997-10-17
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Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
FILING DATE: 1998-06-25
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Kljavin, Ivar J.
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Botstein, David
Desnoyers, Luc
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Best Local Similarity
Matches 24; Conserv
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US-09-990-562-345
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PRIOR PELLING DATE: 1998-06-04
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065181
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DR APPLICATION NUMBER: 60/091626

DR APPLICATION NUMBER: 60/091633

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Publication No. US20030027162A1
GENERAL INFORMATION:
                   FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
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Gurney, Austin I.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                           FILING DATE: 1998-07-02
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Ferrara, Napoleone
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Goddard, Audrey
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Botstein, David
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                                                                                                                                                                                                                                                                                                                    Query Match 34.3%; Score 112; DB 9; Length 111; Best Local Similarity 42.9%; Pred. No. 0.00014; Matches 24; Conservative 6; Mismatches 24; Indels
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PRIOR PILING DATE: 1997-06-16
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PRIOR PELLING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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Publication No. US20030027163A1
GENERAL INFORMATION:
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Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Botstein, David
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089653
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089599
                       FILING DATE: 1998-05-28
APPLICATION UNMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091544
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C63
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                                                                                                                Query Match 34.3%; Score 112; DB 9; Length 111; Best Local Similarity 42.9%; Pred. No. 0.00014; Matches 24; Conservative 6; Mismatches 24; Indels
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CURRENT FILING DATE: 2001-11.19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062260
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-04-28
PRIOR PELLATION NUMBER: 60/084600
PRIOR PELLATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-28
PRIOR PLING DATE: 1998-05-28
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PRIOR PILING DATE: 1998-06-02
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; Patent No. US20020072067A1
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
PRIOR PPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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FILING DATE: 1998-03-20
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Grimaldi, J. Christopher
Gurney, Austin L.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
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Botstein, David
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R FILING DATE: 1998-06-03
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/088028 APPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/08861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 1998-06-09 ILING DATE: 1998-06-10 FILING DATE: 1998-06-16 ILING DATE: 1998-06-17 FILING DATE: 1998-06-16 1998-06-17 FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: PRIOR

R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
APPLICATION UNMBER: 60/090435
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Query Match 34.3%; Score 112; DB 10; Length 111; Best Local Similarity 42.9%; Pred. No. 0.00014;

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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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FILE REFERENCE: P2730PLGS 201-11-19
FILE REPERING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/06250
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   2; Gaps
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                                                                                          20 AVEGVÆGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
6; Mismatches 24; Indels
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Patent No. US20020072092A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
   24; Conservative
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PRIOR APPLICATION NUMBER: 60/088028
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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PRIOR PILING DATE: 1997-06-16
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PRIOR PELING DATE: 1997-11-12
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065312
PRIOR PELING DATE: 1997-11-24
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                                                 Sequence 345, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Botstein, David
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Eaton, Dan L.
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Tumas, Daniel
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34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels
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R APPLICATION NUMBER: 60/090696
R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-26
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R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090694
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R APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088217
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PPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090252
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Sequence 345, Application US/09989727; Patent No. US20020072497A1; GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.

RESULT 22 US-09-989-727-345

PRIOR PRIOR APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC65 CURRENT APPLICATION NUMBER: US/09/989,727 CURRENT FILING DATE: 2001-11-19 RENT FILING DATE: 2001.11-19

R APPLICATION NUMBER: 60/049787

R APPLICATION NUMBER: 60/062250

R FILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065710

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066770

R FILING DATE: 1997-11-24 FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/08332
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07 RILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 APPLICATION NUMBER: 60/087106 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 Godowski, Paul J. Grimaldi, J. Christopher Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K.
Williams, P. Mickey
Wood, William I. Ferrara, Napoleone 1998-06-04 'ILING DATE: 1998-06-02 Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Gurney, Austin L. Kljavin,Ivar J. Napier,Mary A. Botstein, David Goddard, Audrey Desnoyers, Luc Eaton, Dan L. 'ILING DATE: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT. APPLICANT APPLICANT PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR
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R APPLICATION NUMBER: 60/088655
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R APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089440 CATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090429 APPLICATION NUMBER: 60/088217 1998-06-05 1998-06-10 FILING DATE: 1998-06-19 1998-06-22 1998-06-11 1998-06-12 1998-06-17 FILING DATE: 1998-06-17 FILING DATE: 1998-06-1 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: 

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptices and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC70
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CURRENT APPLICATION NUMBER: G0/049787
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PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/088655
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Paoni, Nicholas F.
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                                                                                                                             Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                           Tumas, Daniel
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42.9%; Pred. No. 0.00014;
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                         APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/092182
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Eaton, Dan L.
Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Gerber, Hanspeter
   FILING DATE: 1998-06-24
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089599
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Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/090535
                                                             CATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090862
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Grimaldi, J.Christopher
Gurney, Austin L.
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Ferrara, Napoleone
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Gerber, Hanspeter
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Napier, Mary A.
Pan, James
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Desnoyers, Luc
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                              Roy, Margaret Ann
Stewart, Timothy A.
Paoni, Nicholas F.
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PRIOR PLING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/09
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| TITLE OF INVESTION | ACCUSAGE ENCODING the Same Polypeptides and Nucleic FITTLE OF INVESTION | ACCUSAGE ENCODING the Same Polypeptides and Nucleic FITTLE OF INVESTION | ACCUSAGE ENCODING the Same FITTLE OF INVESTION | ACCUSAGE ENCODING the Same FITTLE OF INVESTION | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING | ACCUSAGE ENCODING
                Zhang, Zemin
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090676

R APPLICATION NUMBER: 60/090678

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Patent No. US20020127576A1
GENERAL INFORMATION:
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
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FILING DATE: 1998-06-26
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Goddard, Audrey
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Kljavin, Ivar J.
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Botstein, David
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Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel

APPLICANT: APPLICANT:

Paoni, Nicholas F.

Pan,James

Napier, Mary A.

APPLICANT APPLICANT

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.3%; Score 112; DB 10;
Similarity 42.9%; Pred. No. 0.00014;
34; Conservative 6; Mismatches 24;
                                 PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1988-06-25
PRIOR PAPPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1988-06-26
PRIOR PAPLICATION NUMBER: 60/090862
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09180
PRIOR APPLICATION NUMBER: 60/09180
PRIOR APPLICATION NUMBER: 60/09154
PRIOR APPLICATION NUMBER: 60/091549
PRIOR FILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091549
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
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Patent No. US20020132252A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-07-07
PRIOR PPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090694
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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                        1998-06-25
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Eaton, Dan L.
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Best Local Simil
Matches 24;
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US-09-990-442-345
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CURRENT APPLICATION NUMBER: US/09/990,442 CURRENT FILING DATE: 2001-11.14 PRIOR APPLICATION NUMBER: 60/049787

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R APPLICATION NUMBER: 60/086212
R APPLICATION NUMBER: 60/086212
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/08855
R FILING DATE: 1998-06-09
R FILING DATE: 1998-06-09 R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088028

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088029

R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/088861 R FILING DATE: 1998-06-11 R APPLICATION NUMBER: 60/088876 F FILING DATE: 1998-06-11 R APPLICATION NUMBER: 60/089105 R FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/062250 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/087106 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088858 ILING DATE: 1998-05-07 FILING DATE: 1997-10-17 1998-05-28 1998-06-10 FILING DATE: 1998-06-11 FILING DATE: 'ILING DATE: PRAIOR PR

APPLICATION NUMBER: 60/089948 PILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/090557 1998-06-19 1998-06-17 1998-06-17 1998-06-18 1998-06-22 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-25 FILING DATE: 1998-06-25 FILING DATE: 1998-06-24 1998-06-24 FILING DATE: LING DATE: LING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRILICA PRILIC PRIOR PRIOR PRIOR

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                                                                                                                                                                                                                                                                                                        34.3%; Score 112; DB 10; Length 111; 42.9%; Pred. No. 0.00014; ive 6; Mismatches 24; Indels
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CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE. AND APPLICATION TO A CURRENT FILING DATE.
        PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PILING DATE: 1998-07-02
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PRIOR FILING DATE: 1997-06-16
PRIOR PLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
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Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Kljavin, Ivar J.
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Best Local Similarity 42.9°
Matches 24; Conservative
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Desnoyers, Luc
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US-09-991-163-345
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R APPLICATION NUMBER: 60/075945
R FILING DATE: 1998-02-25
A PAPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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APPLICATION UNMBER: 60/089514
APPLICATION DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088029
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APPLICATION UNDRER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/08861
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/0
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089509
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-25
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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34.3%; Score 112; DB 10;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24;
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CURRENT APPLICATION NUMBER: US/09/993,604

CURRENT FAPLICATION NUMBER: US/09/993,604

CURRENT FILING DATE: 2001-11-14

PRIOR PELLORATION NUMBER: 60/649787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PELLORATION NUMBER: 60/66510

PRIOR FILING DATE: 1997-11-12

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PRIOR APPLICATION NUMBER: 60/065910

PRIOR APPLICATION NUMBER: 60/05910

PRIOR APPLICATION NUMBER: 60/079910

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PRIOR APPLICATION NUMBER: 60/079312
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Grimaldi, J. Christopher
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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PRIOR PILING DATE: 1998-04-08
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R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

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R FILING DATE: 1998-06-24

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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R APPLICATION NUMBER: 60/091544 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-66-22 PPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/089948 ILING DATE: 1998-06-24 FILING DATE: 1998-06-24 

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 0.00014;
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34.3%; Score 112; DB
Best Local Similarity 42.9%; Pred. No. 0.00
Matches 24; Conservative 6; Mismatches
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CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001.11.14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
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R APPLICATION NUMBER: 60/05945
R FILING DATE: 1997-11-24
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Patent No. US20020137890A1
GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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FILING DATE: 1998-06-02
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
                                                  2; Gaps
                                                                                                    1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                           20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
  Length 111;
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Score 112; DB 10;
Pred. No. 0.00014;
6; Mismatches 24;
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CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

PRIOR PEDILCATION NUMBER: 60/049787

PRIOR PEDILCATION NUMBER: 60/06250

PRIOR PELLING DATE: 1997-06-16

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                                                                                                                                                                                                                                                                                       Sequence 345, Application US/09989721; Patent No. US20020142961A1; GENERAL INFORMATION:
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Query Match
Best Local Similarity 42.9%;
Matches 24; Conservative
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Gerritsen, Mary E.
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Pan, James
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US-09-989-721-345
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R APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/0
FILLING DATE: 1998-06-26
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1998-06-19
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APPLICATION NUMBER:
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PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILICA PRILIC
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PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PASLSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 67, Application US/09790264 ; Patent No. US20020028508A1
                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-09-790-264-67
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                                                                                                                                              SEQ ID NO 58
LENGIH: 74
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                                                                                                                  Sequence 59, Application US/09790264

Sequence 59, Application US/09790264

Sequence 59, Application US/09790264

Sequence 59, Application US/09790264

Sequence 50, Application US/09790264

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: MCCarthy, Sean A.

ITILE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

ITILE OF INVENTION: USES

FILE REPERENCE: 0734-32201

CURRENT APPLICATION NUMBER: US 09/790,264

CURRENT FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23

PRIOR PILING DATE: 1999-04-23

PRIOR PILING DATE: 1999-04-23

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: US 09/102,705

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-06-22

PRIOR PLING DATE: 1999-07-29

PRIOR PLING DATE: 1999-07-29

PRIOR PLING DATE: 1999-07-29

PRIOR PLING DATE: 1999-07-29

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Batent No. US2002028508A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: MCCARIAY, Sean A.

ITLE OF INVENTION: PROGNASTIC, PREVENTIVE, THERAPEUTIC, AND OTHER

ITLE OF INVENTION: USES

FILE REFERENCE: 0734-322001

CURRENT APPLICATION NUMBER: US/09/790,264

CURRENT APPLICATION NUMBER: US 09/065,661

PRIOR PILING DATE: 1998-04-23

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-06-22

PRIOR PILING DATE: 1999-06-22

PRIOR PILING DATE: 1999-06-22

PRIOR PILING DATE: 1999-06-22

PRIOR PILING DATE: 1999-06-22

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20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Rattus norvegicus
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Matches 20; Conserv
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
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                                                                          Indels 17;
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                                                                                                                                                     12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                           29 KPGACP-----KPPPRSFGTCDERCTGDGSCSGNMKCCSNGCGHACKPP 72
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       Length 74;
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Query Match 29.5%; Score 96.5; DB 10; Best Local Similarity 37.7%; Pred. No. 0.0031; Matches 20; Conservative 1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE REFENCE: 05334-322001
CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/298,531
PRIOR APPLICATION NUMBER: US 09/298,531
PRIOR APPLICATION NUMBER: US 09/298,363
PRIOR PILING DATE: 1999-04-23
PRIOR PILING DATE: 1999-04-23
PRIOR PILING DATE: 1999-06-22
PRIOR PLILING DATE: 1999-06-22
PRIOR PLILING DATE: 1999-06-22
PRIOR PLILING DATE: 1999-06-22
PRIOR PLILING DATE: 1999-06-22
PRIOR PLILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 68
NUMBER OF SEQ ID NOS: 68
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US-09-992-600A-42
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Patent No. US2002026508A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: MCCARTHY, SEAR A.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER

TITLE OF INVENTION: DATE: 2001-02-21

FILE REPERENCE: 07334-32201

CURRENT APPLICATION NUMBER: US 09/065,661

PRIOR APPLICATION NUMBER: US 09/298,531

PRIOR APPLICATION NUMBER: US 09/298,531

PRIOR FILING DATE: 1998-04-23

PRIOR PLING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR PLING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 68

SEQ ID NOS: 68

SEQ ID NO 56

LENGTH: 76
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28.9%; Score 94.5; DB 10; Length 76;
Best Local Similarity 35.8%; Pred. No. 0.0049;
Matches 19; Conservative 3; Mismatches 14; Indels 1
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Kumble, Anand
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000, 1037c3
CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-790-264-56
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mouse
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US-09-790-264-56
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LENGTH: 72
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| Sequence | 22, Application US (09924340 |
| Sequence | 24, Application US (09924340 |
| Sequence | 24, Application US (09924340 |
| Sequence | 24, Application US (09924340 |
| Semblication US (0900224841 |
| Sequence | 24, Application US (09924340 |
| Sequence | 24, Application US (09924340 |
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| TILLE OF INVENTION HUMBAN CDMAS AND PROTEINS AND USES THEREOF |
| TILLE OF INVENTION HUMBAN CDMAS AND SEQUENCE |
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APPLICANT: BOUSSI-YANICOSTAS, NADIA
APPLICANT: BOUSSI-YANICOSTAS, NADIA
APPLICANT: BOUSSI-YANICOSTAS, NADIA
APPLICANT: HARDELIN, JEAN-PIERRE
APPLICANT: BARAILH, CATHERINE
APPLICANT: BOUGON, GENEVIEVE
APPLICANT: BOUGON, GENEVIEVE
APPLICANT: BOUGON, GENEVIEVE
APPLICANT: MAZIE, JEAN-CLAUDE
TITLE OF INVENTION: THERABEUTIC COMPOSITION COMPRISING KAL PROTEIN AND USE
TITLE OF INVENTION: OF THE KAL PROTEIN FOR THE TREATMENT OF RETINAL, RENAL,
TITLE OF INVENTION: NEURONAL AND NEURAL INJURY
FILE REFERENCE: 0660-0151-0XPCT
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US/09/319,236
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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28.3%; Score 92.5; DB 12; Length 679;
Best Local Similarity 34.6%; Pred. No. 0.056;
Matches 18; Conservative 3; Mismatches 20; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.4%; Score 93; DB 10; Length 137; 40.4%; Pred. No. 0.012; Live 6; Mismatches 20; Indels
28.4%; Score 93; DB 9; Length 124; 40.4%; Pred. No. 0.011; tive 6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                            TTLE OF INVENTION: Nucleic Acids, Proteins and Antibodies ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PLING DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                            76 KEGSCPQVNINFPQLGLCRDQCQVDSQCPGQMKCCRNGCGKVSCVTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 KEGSCPQVNINFPQLGLCRDQCQVDSQCPGQMKCCRNGCGKVSCVTP 135
                                                                                                           12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                                                                                            Sequence 1361, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/10119714; Patent No. US20020123467A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.4%
Matches 19; Conservative
                         Best Local Similarity 40.49
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1361
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                         US-09-925-300-1361
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LENGTH: 679
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US-10-119-714-1
  Query Match
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                                                    130 KOGDCPAPEKASGFAAACV----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.0%; Score 85; DB 9; Length 133; 40.4%; Pred. No. 0.068; tive 2; Mismatches 25; Indels
12 KPGSCPI----ILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
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                                                                                                                                                                                                                                                                              TITLE OF INVENTION: 28 Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins CURRENT Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PEOOBPE
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
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PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR PILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR PILING DATE: 1997-05-06-06
PRIOR PILING DATE: 1997-12-19
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR PLING DATE: 1998-09-11
PRIOR PLING DATE: 1998-09-11
PRIOR FILING DATE: 1998-03-12
                                                                                                                                                                                                   Sequence 75, Application US/09852797; Patent No. US20020172994A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-853-161-75
; Sequence 75. Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens US-09-852-797-75
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Best Local Similarity
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 26.0%; Score 85; DB 10; Length 133;
1 Similarity 40.4%; Pred. No. 0.068;
21; Conservative 2; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: 28 Human Secreted Proteins; TITLE OF INVENTION: 28 Human Secreted Proteins; TITLE OF INVENTION: 28 Human Secreted Proteins; FILE REFERENCE: PSOOSP4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 06/265,583
PRIOR APPLICATION NUMBER: 06/265,583
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-05-30
PRIOR PRIOR DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR PILING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 21; Conservat
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LENGTH: 133
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                                                                                                                                                                                                                                                                                                                                                                                 19 VQGPGLTDWLFPRRCPKÍREECE-FQERDVCTKDRQCQDNKKCCVFSCGKKC 69
                                                                                                                        Query Match 26.0%; Score 85; DB 10; Length 133; Best Local Similarity 40.4%; Pred. No. 0.068; Matches 21; Conservative 2; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                      5 VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC
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Best Local Similarity 42.5%; Pred. No. 0.17;
Matches 17; Conservative 1; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT PILING DATE: 2001-05-11
PRIOR PELICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-14
PRIOR PILING DATE: 1998-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GRCPKIREECE-FQERDVCTKDRQCQDNKKCCVFSCGKKC 53
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
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; Patent No. US20020077287A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 119, Application US/09852659A; Patent No. US20020077287A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
: Homo sapiens
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US-09-852-659A-119
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                                        US-09-852-659A-75
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TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FURRENT PRILIGE OF 104-238
FRIOR APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NOS: 506
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 250, Application US/09894882; Patent No. US20020102607A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones, Robert M.
Shen, Greg S.
                                                             TYPE: PRT
CRGANISM: Conus emaciatus
US-09-894-882-241
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   SEQ ID NO 241
LENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.1%; Score 75.5; DB 10; Length 102; 42.1%; Pred. No. 0.45; tive 1; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CPKIREECE-FQERDVCTKDRQCQDNKKCCVFSCGKKC 38
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/
PRIOR PELICATION NUMBER: US 60/243,410
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
                PRIOR PELICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR PELICATION NUMBER: 60/265,583
PRIOR PLING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-03-12
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-05-30
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PRIOR PELING DATE: 1997-05-05
PRIOR PELING DATE: 1997-05-06
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PRIOR PELING DATE: 1997-05-06
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Patent No. US20020102607A1
GENERAL INFORMATION:
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APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jones, Rohe.
TITT:
CURRENT FILING DATE: 2001-05-11
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Walker, Craig S.
Shetty, Reshma
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Best Local Similarity 42.1%
Matches 16; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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                                                                   7;
Query Match 22.5%; Score 73.5; DB 10; Length 70; Best Local Similarity 37.5%; Pred. No. 0.5; Matches 18; Conservative 8; Mismatches 15; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.5%; Score 73.5; DB 10; Length 70; Best Local Similarity 37.5%; Pred. No. 0.5; Matches 18; Conservative 8; Mismatches 15; Indels 7.
                                                                                                                                                                             9 SCFLLVIVCLNLIVLINACYQDETPCRGSIFCCRKKCCIGTCRFPCYV 56
                                                                                                                                  15 SCPIILIRCA-MINPPNRCLKD-TDCPGI-----KKCCEGSCGMACFV 55
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APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
FILE REFERENCE: 00-25
CURRENT APPLICATION NUMBER: US/09/819,136
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/193,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Mointosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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ORGANISM: Homo sapiens
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ORGANISM:
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                                                                                Gaps
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                                                                                            9 VSTKPGSCPIILIRCAMINP------PNRCLKDTDCPGIKKCCEGSCGM 51
                                                               Query Match 22.0%; Score 72; DB 10; Length 548; Best Local Similarity 28.3%; Pred. No. 4.5; Matches 15; Conservative 6; Mismatches 16; Indels
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 548
                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                       US-09-864-761-34921
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LENGTH: 49
                                                  US-09-819-136-2
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OTHER INFORMATION: MAP TO AL050348.19
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EST HUMAN HIT: BF197609.1, EVALUE 1.00e-25
US-09-864-761-34921
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19.7%; Score 64.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 3.7;
Matches 15; Conservative 6; Mismatches 19; Indels 9
                                                                                                                                                                                                                                                                                                           21.1%; Score 69; DB 10; Length 49; 40.0%; Pred. No. 0.99;
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                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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APPLICANT: Malker, Craig S.
APPLICANT: Shetty, Reshma.
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-10-29

NUMBER OF SEQ ID NOS: 506

SOFTWARE: PatentIn version 3.0

SEQ ID NO 244

LENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                     32 CLKDTDCPGIKKCCEGSCGMACFVP 56
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Best Local Similarity 40.05
Matches 10; Conservative
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6; Mismatches
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TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-350
                                                                                                          Query Match
Best Local Similarity 26.48
Matches 14; Conservative
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Walker, Craig S.
Shetty, Reshma
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US-09-894-882-476
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19.7%; Score 64.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 3.7;
Matches 15; Conservative 6; Mismatches 19; Indels
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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Walker, Inc.
APPLICANT: Jimenez, Esha C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
                                                                         APPLICANT: Sincly, Meshind
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/29
FRIOR APPLICATION NUMBER: US 60/29
FRIOR APPLICATION NUMBER: US 60/243,410
FRIOR FILING DATE: 2000-10-27
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
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FRIOR FILING DATE: 2001-01-29
FRIOR FILING DATE: 2001-01-29
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APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/9894,882
CURRENT APPLICATION NUMBER: US 60/249
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-08
PRIOR PRILING DATE: 2000-11-08
PRIOR PRILING DATE: 2000-11-04
PRIOR PRILING DATE: 2000-11-04
PRIOR FILING DATE: 2000-11-04
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE PARCENTIN VUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
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US-09-894-882-256
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LENGTH: 70
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19.7%; Score 64.5; DB 10; Length 70; 26.4%; Pred. No. 3.7; tive 8; Mismatches 24; Indels 7
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APPLICANT: Olivera, Baldometo M.
APPLICANT: Olivera, Baldometo M.
APPLICANT: Olivera, Baldometo M.
APPLICANT: Olivera, Baldometo M.
APPLICANT: Watkins, Maren
APPLICANT: Wichard David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Jones, Robert M.
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; APPLICANT: University of Utah Research Foundation
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Best Local Similarity 38.2%; Pred. No. 4;
Matches 13; Conservative 2; Mismatches 17; Indels
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18.7%; Score 61; DB 10; Length 44;
Best Local Similarity 43.3%; Pred. No. 5.4;
Matches 13; Conservative 3; Mismatches 8; Indels
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2000-66-39
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR PILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin Version 3.0
SEQ ID NO 459
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
SOFTWARE: PARENTIN NUMBER: US 60/264,256
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PARENTIN VETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
MoIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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US-09-894-882-476
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TYPE: PRT
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                                                 Sequence 462, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Carig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Matkins, Maren
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE BEFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR PLILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLILING DATE: 2000-11-08
PRIOR PLILING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2001-11-04
PRIOR PELING DATE: 2001-11-04
PRIOR PELING DATE: 2001-11-04
PRIOR PELING DATE: 2001-11-04
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 506
SEOTHARE: PALENTIN VETSION 3.0
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APPLICANT: Shen, Greg S.
FILLE OF INVENTION: 1-Superfamily Conotoxins
FILE REPERENCE: 2314-238
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-37
PRIOR PELICATION NUMBER: US 60/243,410
PRIOR PELICATION NUMBER: US 60/246,581
PRIOR PELICATION NUMBER: US 60/246,581
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; Patent No. US20020102607A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-462
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RESULT 55
US-09-894-882-462
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                                                                                                                                                                                                                                                                                                                   18.7%; Score 61; DB 10; Length 44; 43.3%; Pred. No. 5.4; 8; Indels vative 3; Mismatches 8; Indels
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; Patent No. US20020102607A1
; GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
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APPLICANT: Jones, RODELL ...
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REPERBENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/244,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CYQDETPCRGSTFCCRKKCCIGTCRFPCYV 30
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PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 489, Application US/09894882 Patent No. US20020102607A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jimenez, Elsie C.
PPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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Walker, Craig S.
Shetty, Reshma
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.3%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Conus emaciatus
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9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SCPIILIRCA-MLNPPNRCLKD-----TDCPGIKKCCEGSCGMACFV 55
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TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REPRENENCE: 2.314-2.95
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
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PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
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Walker, Craig S.
Shetty, Reshma
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US-09-894-882-253
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APPLICANT:
APPLICANT:
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APPLICANT:
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18.2%; Score 59.5; DB 10; Length 69; 35.7%; Pred. No. 11; tive 8; Mismatches 14; Indels
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18.0%; Score 59; DB 10; Length 32;
Best Local Similarity 38.2%; Pred. No. 6.3;
Matches 13; Conservative 1; Mismatches 18; Indels
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        APPLICANT: Shen, Greg S.

TITLE OF INVENTION: 1.28uperfamily Conctoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-34
PRIOR PILING DATE: 2000-11-34
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PALENTIN VETSION 3.0
SEQ ID NO 265
LENGTH: 69
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APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Watkins, Maren
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-238
FILE REFERENCE: 2114-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
FRIOR APPLICATION NUMBER: US 60/243,410
FRIOR FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: US 60/243,410
FRIOR PELING DATE: 2000-10-27
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
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FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
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Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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5 SOFTWARE: Patentin version 3.0

5 SEQ ID NO 477

LENGTH: 32

7 TYPE: PRT

ORGANISM: Conus episcopatus
US-09-894-882-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 35,7
Matches 15, Conservative
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ORGANISM: Conus virgo
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Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 17; Indels
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Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                            15 SCPIILIRCA-MLNPPNRCLKD-----TDCPGIKKCCEGSCGMACFV 55
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APPLICANT: University of Utah Research Foundation
APPLICANT: Canid S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Michael
APPLICANT: Matkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Warker, Craig S.
APPLICANT: Marker, Craig S.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Markins, Maren
APPLICANT: Warkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shoet, Maren
APPLICANT: Shoet, Evg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/249
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PRILING DATE: 2000-11-04
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PRILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 262, Application US/09894882; Patent No. US20020102607A1; GENERAL INFORMATION:
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Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-253
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APPLICANT:
APPLICANT:
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Jones, Robert M.

APPLICANT: APPLICANT:

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APPLICANT:

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GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.;
APPLICANT: Graig S.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Eslie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Markins, Marki
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TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: P8723P1
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
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PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR PILING DATE: 2001-01-17
PRIOR PLING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 60/19,065
PRIOR FILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PLILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-09-12
SUMMBER OF SEQ ID NOS: 97
SOFTWARE: PATCHILIN Ver. 2.0
PRIOR FILING DATE: 2000-10-2/
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR PILING DATE: 2010-10-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 353
LENGTH: 70
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// Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 97, Application US/09915582; Patent No. US20020120103A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Conus episcopatus US-09-894-882-353
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Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
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FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PLILING DATE: 2000-06-30
PRIOR PLLING DATE: 2000-10-27
PRIOR PLLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-37
PRIOR PLLING DATE: 2000-11-37
PRIOR PLLING DATE: 2000-11-37
PRIOR APPLICATION NUMBER: US 60/245,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-34
PRIOR FILING DATE: 2001-11-3
PRIOR FILING DATE: 2001-11-3
NUMBER: OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
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                  23 CAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                       1 CAGQEEP--CSSRDDCCGSVGCCFGQCETPCRMP 32
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
                                                                                                                                                                                                                                                          Sequence 286, Application US/09894882 Patent No. US20020102607A1 GENERAL INFORMATION:
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Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Shen, Greg S.
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US-09-894-882-286
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APPLICANT:
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18.0%; Score 59; DB 10; Length 173;
Best Local Similarity 31.0%; Pred. No. 29;
Matches 18; Conservative 8; Mismatches 22; Indels 10; Gaps
                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 AQGSVRGPATPWQGSCTSIISCLRAPDPPPGTTLVGLRLEGKECQNSSPGGRRVCEPS 125
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Query Match 18.0%; Score 59; DB 10; Length 70; Best Local Similarity 38.2%; Pred. No. 13; Matches 13; Conservative 1; Mismatches 18; Indels
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LOCATION: (1)...(44)
CTHER INFORMATION: Kaa at residues 7, 27 and 44 is Pro or hydroxy-Pro; Kaa at residu OTHER INFORMATION: es 5, 33 and 39 is Glu or gamma-carboxy-Glu; Kaa at residues 2 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: SWISSEROT HIT: PO2438, EVALUE 4.00e-03

OTHER INFORMATION: EST_HUMAN HIT: W76571.1, EVALUE 4.00e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PGSYPSSLVYSTALCSPSTCQLRSSLYRDCQ--kTCWEPASCQKSCYRPR 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Indels
                 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 42841
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APPLICANT: University of Utah Research Foundation
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE FEFERENCE: 2314-238
CURRENT PAPLICATION NUMBER: US/09/894,882
CURRENT PILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US 60/243,410
FRIOR PELLING DATE: 2000-06-30
FRIOR PELLING DATE: 2000-10-27
FRIOR PELLING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-01-09
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FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-01-09
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17.9%; Score 58.5; Di
Best Local Similarity 36.0%; Pred. No. 17;
Matches 18; Conservative 7; Mismatches
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; Patent No. US20020102607A1
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Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                     LENGTH:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REPRENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/894,882
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
SEQ ID NO 232
LENGTH: 69
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US-09-894-882-232
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US-09-815-242-10742
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OTHER INFORMATION: Xaa at residues 7, 27 and 44 is Pro or hydroxy-Pro; Xaa at residu OTHER INFORMATION: es 5, 33 and 39 is Glu or gamma-carboxy-Glu; Xaa at residues 2 an OTHER INFORMATION: d 29 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr OTHER INFORMATION: r O-phospho-Ty
; OTHER INFORMATION: d 29 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr; OTHER INFORMATION: r O-phospho-Ty US-09-894-882-242
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                                                                                          17.7%; Score 58; DB 10; Length 44; 43.3%; Pred. No. 10; tive 2; Mismatches 9; Indels
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-04
PRIOR FILING DATE: 2000-11-04
PRIOR FILING DATE: 2000-11-04
PRIOR FILING DATE: 2000-11-04
PRIOR FILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 506
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.7%; Score 58; UB Best Local Similarity 43.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 CLKD-TDCPGI----KKCCEGSCGMACFV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXODXTXCRGSTFCCRKKCCIGTCRFXCXV 30
                                                                                                                                                                                       32 CLKD-TDCPGI----KKCCEGSCGMACFV 55
                                                                                                                                                                                                                            1 CXQDXTXCRGSIFCCRKKCCIGTCRFXCXV 30
                                                                                                                                                                                                                                                                                                                                            Sequence 251, Application US/09894882
Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10012076; Patent No. US20020151472A1; GENERAL INFORMATION: APPLICANT: Lars, Thim
                                                                                                                                                                                                                                                                                                                                                                                                                               Cognetix, Inc.
Walker, Craig S.
Shetry, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
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Jones, Robert M.
Shen, Greg S.
                                                                                                                      Local Similarity 43.33
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APPLICANT: Poulsen, Steer Sloth
APPLICANT: Poulsen, Steer Sloth
TITLE OF INVENTION TYPE Epities
FILE RESERVENCE: 6256.500 US
CUURRENT FILMS DATE: 2001-12-07
FILE RESERVENCE: 6256.500 US
FILE RESERVENCE: 6256.500 US
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Shetty, Reshma
Jimenez, Elsie C.
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; ORGANISM: Conus figulinus
US-09-894-882-472
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ORGANISM: Conus figulinus
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APPLICANT:
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Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 2; Mismatches 9; Indels 1
  ch 17.7%; Score 58; DB 10; Length 384; l Similarity 44.8%; Pred. No. 74; 13; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,900
CLASSIFICATION: UNMER: US/09/086,900
CLASSIFICATION: UNKnown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/896,449
FILING DATE: 18-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, Deann F.
REFERENCE/DOCKET NUMBER: 2115-001226
                                                                                                                                                                                                                                                                                                                          Yuzbasiyan-Gurkan, Vilma
Schall, William D
Brewer, George J
TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
FACTOR AND METHODS OF USE
                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2199 CAMSCPPSLVYNHC--EHGCP---RLCEGNTSSCGDQPSEGCFCP 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 CAMLNPP----NRCLKDTDCPGIKKCCEG---SCG----MACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: 5445 Corporate Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 472, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-886-900-2
                                                                                     30 NRCLKDTDCPGIKKCCEG--SCGMACFVP 56
                                                                                                                                67 NHDVMDNDAEGIKVMSEGLLSCGVTSFLP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 248-641-1600
TELEFAX: 248-641-0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2813 amino acids
                                                                                                                                                                                                                                     Sequence 2, Application US/09886900 Patent No. US20020137051A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      APPLICANT: Venta, Patrick J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 287637
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Walker, Craig S.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Troy
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Query Match
Best Local Similarity
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                                          Matches
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Search completed: February 11, 2003, 08:46:46 Job time: 99 secs

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Human leukocyte el
Elafin derivative
pPICS/ELEZEL CDNA
Elafin derivative
Elafin. Synthetic
Porcine elafin FLE
Human FLE peptide.
                                                                                                                                      Pebruary 11, 2003, 08:35:56 ; Search time 36 Seconds
(without alignments)
210.980 Million cell updates/sec
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| SIDSZ/gcgd
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/SlDs2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                       908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 100 summaries
                                                                                            OM protein - protein search, using sw model
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AAW57237
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB seq
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Perfect score:
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11 179.5 54.9 189 15 AANSO 334 174.5 54.3 189 15 AANSO 334 174.5 55.4 19 189 15 AANSO 334 174.5 55.4 19 189 15 AANSO 334 174.5 55.4 19 22 14.9 22 AANSO 309 16 16 49.2 126 20 AANSO 309 16 16 49.2 126 20 AANSO 309 16 1747 45.0 6 15 AANSO 309 1747 45.0 6 15 AANSO 309 1745 44.6 6 15 AANSO 309 1745 44.6 6 15 AANSO 309 1745 44.6 6 15 AANSO 309 1745 44.6 6 15 AANSO 309 1745 44.7 6 6 15 AANSO 309 1745 44.7 6 6 15 AANSO 309 1745 44.7 6 6 15 AANSO 309 1745 44.7 6 6 15 AANSO 309 1745 44.7 6 6 15 AANSO 309 1745 44.7 6 174 4	PAI peptide. Su	dium potassiu	iscellaneous pep	se IMC carci	l analogue (	analogue Homo ea	I analoque (	ileukoprotea	leukopr ne prot	ncated SLPI pr	Secretory leukocy	ice of prot	procease in	tic protei	מי	polymorphon	Human serine prote Serine protease in	ombinant serin	I native matur	an seine or	Human serine prote	Serine protease in Semience of protei	Secr	Leukocyte protease	SLPI native immatu Human antileukonro	Human Antileukopro	SLAP1 fusion prote	rSLAP1 iusion prot Serine protease in	Human polymorphonu	-terminal se inhihi	coagulation	skoprotea	Antileukoprotease Serine protease in	ikoprotease	ikoprotea ikoprotea	kidation-re	kidation 31.PT nen	inant secre	#1 of sec	#3 of secr	#4 of se	ss 5-102 o	ic sequenc	stase-inhibit	secretory leukocyt Secretory leukocyt	peptide frag	ileukoprote ine protese	stase-inhibiti	retory leukocy	retory 1 voeptide	retory Leukocy	ues 57-107 o n #1 of secr	
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SPAI pre-sequence

AAY49447 AAE04337 AAE23762 AAR50335

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				ALIGNMENTS	
ULT 1 08217					
AR08217 s	tandard; p	protei	'n.	57 AA.	
AAR08217;					
06-MAR-1991	(first (	entry)	ç		
Human leukocy	cyte elast	astase	inh	inhibiting peptide.	-
Emphysemia; rathritis; cy	espira stic f	tory d	dist is;	ress syndrome; atherosclero: leukaemia.	sis;
Homo sapiens.					
EP402068-A.					
12-DEC-1990.					
04-JUN-1990;	90EP-(	-030603	37.		
02-NOV-1989; 09-JUN-1989; 09-JUN-1989; 25-SEP-1989;	89GB-( 89GB-( 89GB-( 89GB-(	-00247 -00133 -00133	717. 146. 149.		
(ICIL ) IMPER	IAL CHEM	INDS		PLC.	
Christophers	E, Schi	Schroder	MD .	, Pioli D, Wiedow O, Edge	e MD;
WPI; 1990-370 N-PSDB; AAQ06	70081/50. 106819, AA(	50. AAQ06820			
Human leucocytolypoptide fo	ce el	lastase reatment	inh of	inhibitor - is genetically engi: of inflammatory, pulmonary and	engineered and skin
Disclosure, F.	ig 13;	45pp;	Engl	glish.	
Gene product has inhibitory elastase (HLE) and may be is sequence may be expressed frasystem and may be useful in associated with emphysema, a psoriasis and bullous dermatinclude atherosclerosis, cys non-lymphoblastic leukaemia.	has inhibitory;) and may be ibe expressed for the mapping the membry semal in the mmphy semal in the month of the colorests, cy the polypertial public leukaemia.	lbitc ssec sful sful sema s dex sis, lyper	isolatics isolatics isolatics isolatics in the in the imatose cystic cystic in in it.	ivity against humaned from psoriatic a plasmid transform prevention of tiss prevention of tiss other treatable fibrosis, bronchild be used in determining the prevention of th	a leukocyte scales. The ned expression sue damage ress syndrome, conditions is and acute

SX CCC CCC X S X F F F F X X B

Abs raised to the polypeptide may be used in detection.

57 AA;

Seguence

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                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                  1 AQEPVKGPVSTKPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
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                                                            1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant modified elafin with improved oxidation stability has pharmaceutical use as an elastase inhibitor
                                                                                                                                                                                                                                                                                         Elafin, derivative, mutation, transformation, E. coli, yeast, Bacillus subtilis, elastase inhibitor; oxidation.
 Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshida M;
100.0%; Score 327; DB 11;
100.0%; Pred. No. 3.4e-27;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57237 standard; Protein; 142 AA.
                                                                                                                                                                   AAR48552 standard; Protein; 57 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 23; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaji A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0234085.
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                               Conservative
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                                                                                                                                                                                                                                                            Elafin derivative Leu25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TSUR ) TSUMURA & CO.
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es 56; Conserv
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1992;
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                               57;
                                                                                                                                                                                                                                                                                                                                       Synthetic.
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The present sequence represents the protein from the pPIC9/ELF25L cDNA construct containing the elafin 25L gene, used in an example of the present invention. The present invention describes: (1) an elafin (EL) expression vector comprising a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a gene encoding EL and a first region homologous to the genomic DNA of the host (b) a prometer region of (AOCR) gene; (c) a gene encoding signal peptide; (d) a linker designed to secrete a matured elafin; (e) a gene encoding EL; (f) selection marker gene; (g) stop codon, and (h) a second region homologous to a part of the genomic DNA of the host, and (4) a microbial host transformed with the DNA fragment of (3). The microbial hosts can be used to prepare EL commercially. The production of EL by the microbial hosts can be carried on a large scale.
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                                                                                                                                                                                                                                                                                                                                                                                                                               New elafin expression vector - used to transform microbial host(s) for production of elafin commercially
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               Elafin, elafin 25L gene; Pichia pastoris, expression vector, alcohol oxidase 1; controlling region; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%; Score 324; DB 19; Length 142; 98.2%; Pred. No. 1.7e-26; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 11-15; 21pp; Japanese
                                                                                                                 Location/Qualifiers
                                                                                                                                                               86..142
/label= elafin_25L
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                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-340667/30.
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                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV28852
                                                                                  ichia pastoris
                                                                                                                                                                                                               JP10127292-A.
                                                                                                                                                                                                                                                                               31-OCT-1996;
                                                                                                                                                                                                                                                                                                               31-OCT-1996;
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                                                             Synthetic
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                                                                                                                             Peptide
                                                                                                                                                               Protein
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The sequences given in AAR48552-54 represent elafin derivatives. The DNA encoding wild type elafin is mutated, inserted into a suitable vector and then used to transform E. coli, yeast. Bacillus subtilis or animal cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elastase inhibitor activity. They have improved oxidation stability over natural elafin and thus retain activity better under oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AQEPVKGPVSTKPGSCPIILIRCAVLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPO 57
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                                                                                                                                                                                        Recombinant modified elafin with improved oxidation stability has pharmaceutical use as an elastase inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 57;
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                                                                                                                           Yoshida M;
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0
                                                                                                                                                                                                                                                                                                                                                                                              Score 323; DB 15;
Pred. No. 9e-27;
1; Mismatches 0;
                                                                                                                           Okawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR48554 standard; Protein; 57 AA
                                                                                                                                                                                                                              Claim 1; Page 24; 35pp; Japanese.
                                                                                                                           Kaji A,
                                                                                                                                                                                                                                                                                                                                                                                                98.8%;
98.2%;
                                                  93WO-JP01133
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                                                                                                                                                                                                                                                                                                                                                                                                                       56; Conservative
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                                                                                                                           Amagaya S, Ishima Y,
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                                                                                                  (TSUR ) TSUMURA & CO
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Best Local Similarity
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                                                  11-AUG-1993;
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WO9404697-A.
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RESULT 8
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                                      The sequences given in AAR4852-54 represent elafin derivatives. The DNA encoding wild type elafin is mutated, inserted inco a suitable vector and then used to transform E. coli, yeast, Bacillus subtilis or animal cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elastsee inhibitor activity. They have improved oxidation stability over natural elafin and thus retain activity better under oxidative
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                                                                                                                                                                                                                                                                                                                                                                              1 AQEPVKGPVSTKPGSCPIILIRCAILNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                       1 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elafin, elafin 25L gene; Pichia pastoris; expression vector; alcohol oxidase 1; controlling region; promoter.
                                                                                                                                                                                                                                                                     98.8%; Score 323; DB 15; Length 57; 98.2%; Pred. No. 9e-27;
                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Leu, Ile, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57223 standard; Protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 11; 21pp; Japanese.
Claim 1; Page 25; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0304233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0304233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                        Best Local Similarity 98.28
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TSUR ) TSUMURA & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-340667/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 25
                                                                                                                                                                                                                              57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on a large scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pichia pastoris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP10127292-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57223;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
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Proteinase inhibitor; disulfide core proteinase inhibitor; Zdsc1; mouse; pancreatitis; shock syndrome; hyperfibrinolytic hemorrhage; gene therapy; myocardial infarction; antiinflammatory; vasotropic; cardiant; elafin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a new class of proteinase inhibitors called disulfide core proteinase inhibitors (ZdSc1) and provides murine and human ZdSc1 polypeptides. The disulfide core proteins are proteinase inhibitors used for the treament of acute pancreatits, various stages of shock syndrome, hyperfibrinolytic hemorrhage and myocardial infarction. Antagonists of the polypeptides can be used as research reagents for characterizing sites of ligand-receptor interaction. Antibodies against the protein sused for tagging cells that express the protein, for detecting the protein, and for screening expression libraries. Polynucleotides encoding the polypeptides can be used in gene therapy applications where it is desired to increase or inhibit the protein activity. The present sequence represents a porcine elafin, FLE used in homology studies with ZdSc1 polypeptides.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                           57
                                                                                                                                                                                                                              1 AQEPVKGPVSTYRPGSCPIILIRCAXLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                               . 0
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0
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                                                      Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide sequences used as proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                               Indels
                                                  98.2%; Score 321; DB 19;
98.2%; Pred. No. 1.5e-26;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 1.6e-17; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porcine elafin FLE polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 17; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              AAY49447 standard; peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US12545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-072884/06.
                                                                                     Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 AA;
57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY49447;
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Sequence
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                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                    RESULT 7
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AAE04337

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98US-088136P.
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               10-JAN-2001; 2001US-0757908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAI pre-sequence peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 40; Conservative
                                                                                      (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                WPI; 2002-415219/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAI; sodium ion, vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EISA ) EISAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                         04-JUN-1998;
04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP06049098-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1992;
                                                                                                                  Conklin DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR50335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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                                                                                                                        Human, antiinflammatory, vasotropic, cardiant, haemostatic, Zdscl, disulphide core protein, serine proteinase inhibitor, acute pancreatitis, shock syndrome, hyperfibrinolytic haemorrhage, myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human FLE peptide used in the invention. The present invention relates to disulphide core serine proteinase inhibitor Saci protein. Slaci is a member of a new related subfamily referred to as three-disulphide core family. Serine proteinase inhibitors useful for treatment of acute pancreatitis, various states of shock syndrome, hyperfibrinolytic haemorrhage and myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine; disulfide core protein; Zdscl; myocardial infarction; cancer; acute pancreatitis; shock syndrome; transgenic; transgenic animal; hyperfibrinolytic haemorrhage; antisense; gene therapy; vasotropic; antiinflammatory; haemostatic; cardiant; cytostatic; elafin protein; FLE.
                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polypeptides are serine proteinase inhibitors useful for treatment of acute pancreatitis, various states of shock syndrome, hyperfibrinolytic hemorrhage and myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.3%; Score 233; DB 22;
100.0%; Pred. No. 1.6e-17;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IILIRCAMLNPPNRCLKOTDCPGIKKCCEGSCGMACFVPQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Column 9-10, 24pp; English
         AAE04337 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE23762 standard; Protein; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine elafin (FLE) protein.
                                                                                                                                                                                                                                                                             99US-0326039
                                                                                                                                                                                                                                                                                                           98US-0088136
                                                                 04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                     ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-416774/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                              Human FLE peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002052468-A1.
                                                                                                                                                                                                                 US6239254-B1.
                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                            04-JUN-1999;
                                                                                                                                                                                                                                                                                                         04-JUN-1998;
                                                                                                                                                                                                                                                29-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                  Conklin DC;
                                      AAE04337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Matches

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AAE23762

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The present invention relates to novel disulfide core protein (Zdsc1) proteins and polynucleotides encoding such proteins. Zdsc1 sequences are serine proteinses inhibitors. They are used to treat myocardial infarction, acute pencreatitis, various states of shock syndrome, hypertibrinolytic haemorthage and cancer. Zdsc1 sequences and their antibodies can be directly or indirectly conjugated to drugs, toxins and additionable and used for in vivo diagnostic or therapeutic applications. Fusion proteins containing Zdsc1 or their antibodies can be used to target cell or tissue inhibition or ablation, e.g., to treat cancer cells or tissues. Sequences of the invention can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potassium ion, ATP-ase inhibitor peptide; cardiac; PCR; polymerase chain reaction.
New isolated disulfide core protein polypeptide for treating acute pancreatitis, various states of shock syndrome, hyperfibrinolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to produce transgenic or knockout mice. They are also used in gene therapy and antisense gene therapy. The present sequence is porcine elafin protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.3%; Score 233; DB 23;
100.0%; Pred. No. 1.6e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 IILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "pyroglutamyl peptidase"
                                                pancreatitis, various states of shock syndrome
hemorrhage, myocardial infarction, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR50335 standard; Protein; 166 AA.
                                                                                                                                                                     Disclosure; Page 5; 28pp; English.
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127 QDPVKAQPAVPGRFILLSKRGHCPRILFRCPLSNPSNKCWRDYDCPGVKKCCEGFCGKDCL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 61;
                                                                                                                                                                                                                                                                                                                                                                                           /label= Arg or Gly /note= "R when AA 30 = S, G when AA 30 = G" Misc-difference 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Ser or Gly
/note= "S when AA 22 = R, G when AA 22 = G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium potassium ATP inhibiting new peptide - has specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                      Generic sodium potassium ATPase inhibiting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 177.5; DB 13 ilarity 53.4%; Pred. No. 1.5e-11; Conservative 7; Mismatches 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sodium potassium ATPase inhibiting peptide.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1073; 10pp; Japanese.
                                                                                                                                                                 AAR08145 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR08146 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89JP-0086073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of 61 aminoacid(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                    01-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                              Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-365921/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EISA ) EISAI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP02264797-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP02264797-A.
                                                                        187 YPK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Na, K-ATPase
                                                                                                                                                                                                                                                                                                           Na, K-ATPase.
                                       55 VPQ 57
                                                                                                                                                                                                     AAR08145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAI; sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac; vascular disease; PCR; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                              2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACF 54
                                                                                                                        The sequence (AAQ44862) encodes the SPAI peptide which is useful as a drug for treating cardiac and vascular diseases. The peptide is found as a pre-sequence (AARS0335) which is amplified using primers (AAQ44863-67)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence (AAQ44862) encodes the SPAI peptide which is useful as a drug for treating cardiac and vascular diseases. The peptid is found as a pre-sequence (AAR50335) which is amplified using primers (AAQ44863-67)
                                       Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp. DNA - useful to treat cardiac and vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp. DNA - useful to treat cardiac and vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.9%; Score 179.5; DB 15; Length 189; Best Local Similarity 49.2%; Pred. No. 2.8e-11; Matches 31; Conservative 8; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                     54.9%; Score 179.5; DB 15; Length 166; 49.2%; Pred. No. 2.4e-11; tive 8; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR50334 standard; Protein; 189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 6-7; 8pp; Japanese.
                                                                                              Disclosure; Fig 2; 8pp; Japanese.
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                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.29
Matches 31, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-097819/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 AA;
                                                                                                                                                                                                                       166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      164 YPK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPAI peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1994.
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49.2%; Score 161; DB 20; Length 126;
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                                                                                                                                                                                                                                                                                                                                                     AAW98909 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP01592.
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                               27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-080732/07.
                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AA;
                                                                                                                                                       49 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9845431-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                   AAW98909;
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                                                                                                                                                     Sequence
                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                       RESULT 15
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   8×33333333×8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptides composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                    1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                     4 AQPAVPGRFLLSKRGHCPRILFRCPLSNRCWRDYDCPGVKKCCEGFCGKDCLYPK
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                                                                                                                                                                                                                                                          Score 174.5; DB 11; Length 61;
Pred. No. 3.2e-11;
7; Mismatches 19; Indels 1
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                                                                                                                                                    Sodium potassium ATP inhibiting new peptide - has specified sequence of 61 aminoacid(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miscellaneous peptide SEQ ID NO:1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 713; 733pp; English.
                                                                                                                                                                                              Disclosure, Fig 2, 10pp, Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAB92379 standard; Peptide; 49 AA
                                                                                                                                                                                                                                                          ch 53.4%;
1 Similarity 53.4%;
31; Conservative
                               89JP-0086073
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                                                             89JP-0086073
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                                                                                                                      WPI; 1990-365921/49
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                              61 AA;
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                                                                                      (EISA ) EISAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1999;
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                               05-APR-1989;
                                                           05-APR-1989;
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15-OCT-1999;
29-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                              Sequence
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in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;
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useful for screening for potential inhibitors of cancer metastasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SKRGHCPRILFRCPLSNPSNKCWRDYDCPGVKKCCGGKDCLYPK 49
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09-SEP-1993;
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                                                     26-OCT-1994
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor; metastasis associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein associated with cancer metastasis and gene encoding it useful for screening for potential inhibitors of cancer metastasis % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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    52.8%; Pred. No. 1.6e-09;
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                                                Conservative
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Best Local Similarity
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                                                                    Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI; retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme; elastase; cathepsin G; trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI; retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme; elastase; cathepsin G; trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitor - esp. for treating or preventing HIV infection, also new protease inhibitors and nucleic acids encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0943369.
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CLPI analogue (Gly25).
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analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI mol. having only the last 60 amino acids of the native parotid inhibitor. SLPI acts by blocking a host cell enzyme essential for retroviral infection; it is a powerful inhibitor of human leucocyte elastase, cathepain G and human trypsin. The inhibitor provides an effective and relatively safe method for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retroviral infection is inhibited by admin. of an SLPI, or its analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI mol. having only the last 60 amino acids of the native parotid inhibitor. SLPI acts by blocking a host cell enzyme essential for retroviral infection; it is a powerful inhibitor of human leucocyte elastase, cathepsin G and human trypsin. The inhibitor provides an effective and relatively safe method for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI; retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme; elastase; cathepsin G; trypsin.
                                                                                                                                                                                                                                                                              3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting retroviral infection with serine leucocyte protease inhibitor - esp. for treating or preventing HIV infection, also new protease inhibitors and nucleic acids encoding them
                                                     Retroviral infection is inhibited by admin. of an SLPI, or its
                                                                                                                                                                                                                                                                                                          2 DPVDTPTPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP
                                                                                                                                                                                                                44.6%; Score 146; DB 15; Length 60;
48.2%; Pred. No. 3e-08;
Live 4; Mismatches 23; Indels
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48.2%; Pred. No. 3.8e-08;
tive 4; Mismatches 23;
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                     Claim 21; Page 16; 21pp; English.
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                                                                                                                                                                                                                Query Match
Best Local Similarity 48.2
Matches 27; Conservative
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Matches 27; Conservative
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                                                                                                                                                                                  60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    Retroviral infection is inhibited by admin. of an SLPI, or its analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI mol. having only the last 60 amino acids of the native parotid inhibitor. SLPI acts by blocking a host cell enzyme essential for retroviral infection; it is a powerful inhibitor of human leucocyte elastase, cathepsin G and human trypsin. The inhibitor provides an effective and relatively safe method for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI; retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme; elastase; cathepsin G; trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 BPVKGPVST--KPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DPVDTPTPTRRKPGKCPVTYGQCVMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 57
                                                                                                                                        Inhibiting retroviral infection with serine leucocyte protease inhibitor - esp. for treating or preventing HIV infection, also new protease inhibitors and nucleic acids encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting retroviral infection with serine leucocyte protease inhibitor - esp. for treating or preventing HIV infection, also new protease inhibitors and nucleic acids encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      45.0%; Score 147; DB 15; 48.2%; Pred. No. 2.4e-08;
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4; Mismatches
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                                              US DEPT HEALTH & HUMAN SERVICES.
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                                                                              Thompson RC, Wahl SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR51172 standard; Protein; 60 AA
                                                                                                                                                                                                        Claim 25; Page 17; 21pp; English.
 92US-0943369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Conservative
                               SYND ) SYNERGEN INC
                                                                                                            WPI; 1994-118153/14.
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                                                                                                                                                                                                                                                                                                                                                                     60 AA;
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                                                                              Eisenberg S,
 09-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1993;
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                                              USSH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                     Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral; respiratory tract; lung disease; respiratory syncytial virus; RSV; influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tryptase clara inhibitor comprises anti:leuko:protease fragment useful for treatment and prevention of tryptase clara activated viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
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                  DPVDTPTPTRKERFREGKCPVTYGQCFMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.7%; Score 143; DB 18; Length 58; 47.2%; Pred. No. 6e-08; 1ive 3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antileukoprotease derived tryptase clara inhibitor.
                                                                                                                                                                                                          Antileukoprotease derived tryptase clara inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tashiro M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW01844 standard; peptide; 58
                                                                                                              AAW01843 standard; peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kido H,
                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-JP02071.
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                        exosporium glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mumps and measles.
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                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                            28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measles
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                                                                                RESULT 21
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AAW01843-W01851 are peptides derived from the C-terminal portion of human antileukoprotease. The peptides inhibit the action of tryptase clara is responsible for the activation of viruses that have exosporium glycoproteins, such as those that infect the respiratory tract. The peptides are useful for the treatment and prevention of, for example, influenza, parainfluenza, respiratory syncytial virus (RSV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                  Tryptase clara inhibitor comprises anti:leuko:protease fragment useful for treatment and prevention of tryptase clara activated viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
respiratory tract; lung disease; respiratory syncytial virus; RSV; influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
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47.2%; Pred. No. 6e-08;
tive 3; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor peptide sequence.
                                                                                                                                                                                                                               Tashiro M;
                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 20-21; 40pp; Japanese.
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85US-0803471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                               exosporium glycoprotein.
                                                                                                                                                                                                  (TANB ) TOKYO TANABE CO.
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                                                                                                                                                                                                                                                           WPI; 1997-132378/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mumps and measles.
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02-DEC-1985;
29-JUL-1986;
                                                                                                                                                                         24-JUL-1995;
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                                                                                       WO9703694-A1
                                                                                                                                             24-JUL-1996;
                                                            Homo sapiens
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inhibitors f
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05-DEC-1984;
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29-JUL-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB53098 - AAB53122 represent the protease inhibitors Peptide sequences AAB53098 - AAB53122 represent the protease inhibitor of the invention and various orher peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitors protein is useful for treating a protease-mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontiis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                            protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97547 - AAC97541 and AAC97581 and AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligomucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97555 - AAC97573 and AAC9562 - AAC97613 are used in the
                                                                                                                                                                                                                                                                                                                          This invention relates to new purified and isolated mammalian serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                              protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secretory leukocyte protease inhibitor; retroviral; infection; HIV; AIDS; SLPI; CLPI; Parotid inhibitor; antiviral; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serine protease inhibitors and DNA sequences for treating a
                                                                                                           Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Truncated SLPI protein sequence CLPI SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.7%; Score 143; DB 21;
48.2%; Pred. No. 6.2e-08;
                                                                                                           Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                Claim 9; Column 59-60; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY79951 standard; Protein; 60 AA
                                                                                                         Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0943369.
93WO-US08486.
94US-0209040.
  87US-0031846.
87US-0082962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0483503
                                                              (AMGE-) AMGEN BOULDER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                  WPI; 2000-678667/66.
                                                                                                       Bandyopadhyay PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AA;
  30-MAR-1987;
                    04-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6017880-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY79951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY79951
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                                                                                                                                                                                                                                                                                                                                                   retrovirus infection of CD4+ cells comprising contacting the cells with a secretory leukocyte protease inhibitor (SLPI) having the amino acid sequence of a naturally occurring SLPI or a substitution analogue having 107 amino acid residues. SLPI inhibits enzymes whose function are necessary for retroviral infection of the cell. SLPI is a potent inhibitor of elastase, trypsin, cathepsin G and chymotrypsin. The method is useful for treating retrovirus infection in a patient and associated diseases such as acquired immunodeficiancy syndrome (ALDS). The present sequence represents a truncated version of SLPI designated CLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA sequences, useful in recombinant DNA techniques for directing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI.
                                                                                                                                                retrovirus infection using secretory leukocyte protease for treating diseases such as acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                             The present invention describes a method for inhibiting, in vitro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secretory leukocyte protease inhibitor (SLPI) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.7%; Score 143; DB 21;
48.2%; Pred. No. 6.2e-08;
cive 4; Mismatches 23;
   Eisenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by ACA"
                                                                                                                                                                                                                                                                  Disclosure, Column 3-4; 18pp; English.
Wahl SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG65997 standard; Protein; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0031846.
90US-0563832.
94US-0279056.
84US-0678222.
85US-0803471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0890526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
   Dripps DJ, Thompson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Conservative
                                                    WPI; 2000-170378/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-637974/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandyopadhyay PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AA;
                                                                                   N-PSDB; AAZ88483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI67584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                           The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a least one sequence, a Shine-Dalgarno sequence, a ribosome binding site
                                                                                                                                                                                                                                                                                                                                                              or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukcoyte elastase or trypain. The present sequence represents a secretory leukcoyte protease inhibitor (SIPI) analogue that has chymotrypsin and elastase inhibitory activity.
the production of a serine protease inhibitor protein, e.g. leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of protein with the biological activity of HUSI (human seminal plasma inhibitor) type I inhibitors encoded on pRH31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUSI-type inhibitors are useful for treating chronic bronchitis, chronic cervical inflammation, inflammation associated with excessive mucus prodn., post-operative bleeding caused by hyperfibrinolysis, or short. They are esp. suitable for administration as spray or inhalation. The expression control sequence on the DNA fragment in AAN70928 is bound to the 5'-end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EPVKGPVST--KPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protein with human seminal plasma inhibitor activity - ar
new DNA coding sequences, vectors and transformed organisms,
useful eg for treating bronchitis or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 43.7%; Score 143; DB 22; Length 60; Local Similarity 48.2%; Pred. No. 6.2e-08; hes 27; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bronchitis therapy; cervix inflammation; hyperfibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Machleidt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gassen HG,
                                                                                                                Example 9; Column 42; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP70583 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUSI cDNA in an expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86DE-3600571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86DE-3600571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinzel R, Appelhans H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHEF ) GRUNENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-222038/32.
                                          elastase or trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN70929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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construction of DNA encoding the protease inhibitors. Peptide sequences AABS3098 - AABS312 represent the protease inhibitors. Peptide sequences AABS3098 - AABS3122 represent the protease inhibitor of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitor protein as useful for treating a protease mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulomephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97586 - AAC97534, AAC97541 - AAC97581 and AAC976141 represent DNA encoding the protease inhibitors of the invention, and include oligonuclectide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to new purified and isolated mammalian serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                         3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                          32 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New serine protease inhibitors and DNA sequences for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson RC;
43.7%; Score 143; DB 8; Length 90;
                                     Indels
                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor analogue peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stetler GL,
                   Pred. No. 9e-08;
                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 35; Column 65-66; 47pp; English.
                                                                                                                                                                                                         AAB53102 standard; Peptide; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0712354.
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87US-0082962.
                   48.2%;
                                                                                                                                                                                                                                                                                      (first entry)
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-678667/66.
 Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                      27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6132990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1987
                                                                                                                                                                                                                                                AAB53102;
                                                                                                                                                                                                                                                                                                                                                                                                                      elastase.
                                                                                                                                                                         RESULT 27
                                                                                                                                                                                         AAB53102
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43.7%; Score 143; DB 21;

Query Match

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WPI; 1986-169458/26.
  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                            AAP60563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
           ï
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                     Single polypeptide chain protein with at least one active site possessing serine protease inhibitor activity. The protein la resistant to denaturation by heat and acids and is resistant to proteolytic enzymes. It also has the ability to refold following complete reduction of disulphide bonds or denaturation of non-covalent interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor; trypsin-; inhibitor; ss.
                          3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                      33 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic protein capable of directing microbial synthesis of a serine protease inhibitor having similar properties to protein isolated from parotid secretions.
          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%; Score 143; DB 9; Length 106;
48.2%; Pred. No. 1e-07;
ive 4; Mismatches 23; Indels
                                                                                                                                                              serine protease inhibitor; leukocyte elastase inhibitor
Pred. No. 9.1e-08;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP60562 standard; protein; 107 AA
                                                                                       AAP82403 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                   isolated from parotid secretions.
                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 15; 9pp; English.
                                                                                                                                                                                                                                                                                                           serine protease inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                           See also AAP82402 and AAP82597
                                                                                                                                           Serine protease inhibitor #2
nilarity 48.2%;
Conservative
                                                                                                                                                                                                                                                      (SYNE-) SYNERGEN BIOLOGICAL
                                                                                                                                                                                                                   85US-0803423
                                                                                                                                                                                                                                     84US-0678823
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1980 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                         WPI; 1988-227612/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA;
                                                                                                                                                                                                                   02-DEC-1985;
                                                                                                                                                                                                                                    06-DEC-1984;
                                                                                                                                                                                                                                                                        Thompson RC,
                                                                                                                           07-NOV-1990
                                                                                                                                                                               JS4760130-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP60562;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                         AAP82403;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                     RESULT 28
AAP82403
          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
AAP60562
ID AAP6
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The protein directs synthesis of a single chain polypeptide serine protesser-inhibitor, which believed to have at least 2 active sites, 1 exhibiting leukocyte-elasase-inhibiting properties and the other exhibiting activity against trypsin. See also AAN60464-69 and AAP60562-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                           New synthetic DNA sequences for directing microbial synthesis for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence capable of directing microbial synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPVKGPVST - - KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 143; DB 7; Length 107;
Pred. No. 1.1e-07;
4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson RC;
                                                                                                                                                                                                                                                                          Thompson
                                                                                                                                                                                                                                                                          Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secretory leukocyte protease-inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 14; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP60563 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eisenberg SP,
                                                                                                                                                                                                                                                                            Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85WO-US02385.
84US-0678822.
85US-0803471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.2%;
Matches 27; Conservative
                                                                                                                                                        84US-0678822.
85US-0803471.
                                                                                         85WO-US02385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNE-) SYNERGEN BIOLOG INC.
                                                                                                                                       85WO-US02385
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                                                                                                                                                                                                                              (SYNE-) SYNERGEN BIOLOG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin-; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                          WPI; 1986-169458/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA;
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN60463.
                                                                                                                                                                                                                                                                            Sandyopadh PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandyopadh PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1985;
                                                                                         04-DEC-1985;
                                                                                                                                     04-DEC-1985;
                                                                                                                                                          06-DEC-1984;
                                                                                                                                                                                     02-DEC-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO8603519-A.
WO8603519-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1986
                                           19-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Best Loca
Matches
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AAY17426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ϊ,
                                                                                                                                                                 Gaps
                                                                                    The sequence directs synthesis of a secretory leukocyte protease-
inhibitor. See also AAN60463, AAN60465-69 and AAP60562, AAP60564-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and are resistant to proteolytic enzymes. It also has the ability to refold following complete reduction of disulphide bonds or denaturation of non-covalent interactions. See also AAP82402 and AAP82403.
                    New synthetic DNA sequences for directing microbial synthesis for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                          49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single polypeptide chain protein with at least one active site possessing serine protease inhibitor activity. The protein is resistant to denaturation by heat and acids
                                                                                                                                                                                      3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 107;
                                                                                                                                           Length 107
                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                     serine protease inhibitor; leukocyte elastase inhibitor.
                                                                                                                                          Score 143; DB 7;
Pred. No. 1.1e-07;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.7%; Score 143; DB 9;
Best Local Similarity 48.2%; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                               Disclosure; Page 15; 59pp; English.
                                                                                                                                                                                                                                                                AAP82597 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated from parotid secretions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 15; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease inhibitors
                                                                                                                                          43.7%;
                                                                                                                                                                                                                                                                                                                                 serine protease inhibitor #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYNE-) SYNERGEN BIOLOGICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                       85US-0803423
                                                                                                                                                                                                                                                                                                                                                                                                                                           84US-0678823
                                                                                                                                                                                                                                                                                                           07-NOV-1990 (first entry)
                                                                                                                                                    Best Local Similarity 48.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson RC, Ohlsson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1988-227612/32.
                                                                                                                      107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 107 AA;
 N-PSDB; AAN60464.
                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                           US4760130-A.
                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                      AAP82597:
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                          RESULT 31
SX CCX PX TTT XX SX SO SX S
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RESULT 32

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Elastase-inhibiting peptide of low serine protease-inhibiting activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is human polymorphonuclear leukocyte elastase inhibiting protein (SLPI) primary sequence (SLPI is residues 55-107). SLPI has much lower serine protease inhibiting activity. It can be used to treat lung assites tumours, chronic articular rheumatism, gum inflammation, muscular atrophy, allergic lung disease and shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains C-terminal portion of human polymorphonuclear leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; leukocyte elastase inhibitor; parotid secretion; emphysema; serine protease inhibitor; protease/protease inhibitor imbalance; pulmonary disease; polymorphonuclear granulocyte protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EPVKGPVST -- KPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                   human polymorphonuclear leukocyte elastase inhibiting protein.
                                                                                                                          Human polymorphonuclear leukocyte elastase inhibiting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.7%; Score 143; DB 10; Length 107;
48.2%; Pred. No. 1.1e-07;
tive 4; Mismatches 23; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohtsuka E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masuda K,
AAP90384 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY17426 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; page 43; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elastase inhibiting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0283477.
                                                                                                                                                                                                                                                                                                                                                              88WO-JP01342.
                                                                                                                                                                                                                                                                                                                                                                                                      87JP-0330219.
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kamimura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-220549/30.
                                                                                                                                                                    Elastase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
Les 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AA;
                                                                                                                                                                                                                                  Homo sapiens.
                                                                               01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                              28-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1994;
                                                                                                                                                                                                                                                                        WO8906239-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T,
                                                                                                                                                                                                                                                                                                                    13-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5900400-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY17426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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07-JUN-1991;

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2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                26
                                                                                          New serine protease inhibitor protein used in the treatment of
                                                                                                                                                                                                                                                                                                                                       3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                            Ouery Match 43.7%; Score 143; DB 20; Length 107; Best Local Similarity 48.2%; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease inhibitor peptide sequence.
                                                                                                                Claim 25; Column 17; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        AAB53101 standard; Peptide; 107 AA
             85US-0803423.
90US-0581126.
91US-0807769.
94US-0283477.
 88US-0205372
84US-0678823
                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                           27; Conservative
                                                               Thompson RC;
                                                                             WPI; 1999-346413/29.
                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                              107 AA;
10-JUN-1988;
06-DEC-1984;
02-DEC-1985;
10-SEP-1990;
                                   29-JUL-1994;
                            06-DEC-1991
                                                               Ohlsson K,
                                                                                                                                                                                                                                                                                               Seguence
                                                                                                  emphysema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elastase.
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                           RESULT 34
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US6132990-A. 17-OCT-2000.

Synthetic.

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This introlled transce to the protesse inhibitors begins are larged and no more than 107 amino acids. The protesse inhibitors are capable of and no more than 107 amino acids. The protesse inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97524 - AAC97534,

AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protesse inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC9582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors Peptide sequences AAB53098 - AAB53122 represent the protease inhibitors protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a construction, e.g. emphysema, arthritis, glomerulonephritis, periodenticis, muscular dystrophy or tumour invasion. It is also useful construction, e.g. emphysema, arthritis, glomerulonephritis, for modulating protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                               This invention relates to new purified and isolated mammalian serine
                                                                                                                                                                                                                                                        New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor protein; recombinant; leukocyte elastase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.7%; Score 143; DB 21; Length 107;
48.2%; Pred. No. 1.1e-07;
tive 4; Mismatches 23; Indels
                                                                                                                                                                                         Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant serine protease inhibitor protein.
                                                                                                                                                                                         Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                           Claim 23; Column 63; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG65993 standard; Protein; 107 AA
                                                                                                                                                                                      Bandyopadhyay PK, Eisenberg SP,
                                                                85US-0803471.
86US-0890526.
91US-0712354
                                  89US-0293042
                                                                                                   87US-0031846
87US-0082962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0031846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0158085
                                                                                                                                                     (AMGE-) AMGEN BOULDER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Conservative
                                                                                                                                                                                                                          WPI; 2000-678667/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                02-DEC-1985;
29-JUL-1986;
30-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6291662-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2001.
                                                                                                                   04-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG65993
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7;
                                                                                                                                                                                                                                                                                       The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a least one operational element consisting of a promoter, an operator, or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents a recombinant serine protease inhibitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A non-inflammatory vector composition, comprising nucleic acids and antiinflammatory compound, useful for treating inflammatory disorders,
                                                                                                                                                                                            New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                     Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secretory leukoprotease inactivator; SLPI; gene therapy; antiprotease; lung; oxidation resistant; mutation; chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 143; DB 22;
Pred. No. 1.1e-07;
                                                                                                                     Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                           Example 1; Column 7; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47402 standard; protein; 107 AA
                                                                                                                       Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.78;
48.28;
           94US-0279056.
84US-0678222.
85US-0803471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2000; 2000WO-EP13297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0473018
                                                            86US-0890526
90US-0563832
                                                                                                                                                                  N-PSDB; AAI67488, AAI67489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mina M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLPI native mature form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465212/50.
                                                                                                                                                     WPI; 2001-637974/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ennist DL,
                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200148231-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1999;
               22-JUL-1994;
                              05-DEC-1984;
                                                            29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001
                                              02-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47402;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ľu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         datches
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Secretory leukoprotease inhibitor; human; protease inhibitor; malaria; emphysema; asthma; chronic obstructive pulmonary disease; SLPI; cystic fibrosis; otitis media; otitis external; HIV; psoriaais; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
                                                                                        The sequences given in ABB47402-405 represent secretory leukoprotease inactivator (SLPI) proteins which may be used in may be used in gene therapy. SLPI is a major antiprotease present in the lung. A mutation replacing Met/3 of the mature protein with Leu renders the protein oxidation resistant. Therefore it can be used to treat patients with chronic obstructive pulmonary disease (COPD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting procease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease,
                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                          49 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCRRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                                                                                                                  3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                     43.7%; Score 143; DB 22; Length 107; 48.2%; Pred. No. 1.1e-07;
e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secretory leukoprotease inhibitor (SLPI) protein.
                                                                                                                                                                                                                                                                                                               4; Mismatches
                      respiratory distress syndrome and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 32-33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99874 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000US-256699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson HL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-500631/53.
                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                     107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK88016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-2002.
                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr PJ,
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99874
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cystic fibrosis, otitis media, otitis external or HIV infection, or discretaring an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, escama and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the human secretory incorporates inhibitor used to create the fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 BPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                          43.7%; Score 143; DB 23;
48.2%; Pred. No. 1.1e-07;
iive 4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                           107 AA;
                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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       8866666666666666888
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Serine protease inhibitor; human; tumour invasion; macular dystrophy; leukocyte elastase inhibitor; cathepsin G inhibitor; trypsin inhibitor; pancreatic elastase inhibitor; emphysema; rheumatoid arthritis; glomerulonephritis; periodontitis. AAU75058 standard; Protein; 107 AA. Human seine protease inhibitor #1. (first entry) 23-APR-2002 AAU75058; RESULT 38

90US-0581126. 91US-0807769. 94US-0283477. 88US-0205372 .2-JUN-2001; 2001US-0880529 99US-0262828 US2001056180-A1 Homo sapiens .0-JUN-1988; 10-SEP-1990; 06-DEC-1991; 05-MAR-1999; 27-DEC-2001. 29-JUL-1994; 

(AMGE-) AMGEN INC.

Ohlsson K; Thompson RC,

WPI; 2002-121475/16.

Purified serine protease inhibitor proteins isolated from parotid secretions, useful for inhibiting leukocyte elastase, cathepsin G, trypsin and/or pancreatic elastase

Example 3; Page 8; 11pp; English

This invention relates to a novel serine protease inhibitor protein comprising a purified, single-polypeptide-chain protein having at least one active site possessing serine protease inhibitor activity. The protein of the invention has leukocyte elastase inhibitor, cathepsin G inhibitor, trypsin inhibitor and pancreatic elastase inhibitor activities. A disturbance of the protease/protease inhibitor balance may lead to diseases associated with protease-mediated tissue

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glomerulonephritis, periodontitis, macular dystrophy, and tumour invasion. The invention also comprises analogues of the serine protease inhibitors in which the amino acid sequence is varied so as to improve the properties of the protein. These improvements include resistance to oxidative inactivation, improved inhibition of pancreatic present sequence represents the generic serine protease improved inhibition of catheppin G and trypsin. The protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; human; tumour invasion; macular dystrophy; leukocyte elastese inhibitor; cathepsin G inhibitor; trypsin inhibitor; panoreatic elastase inhibitor; emphysema; rheumatoid arthritis; glomerulonephritis; periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel serine protease inhibitor protein comprising a purified, single-polypeptide-chain protein having at least one active site possessing serine protease inhibitor activity. The
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified serine protease inhibitor proteins isolated from parotid secretions, useful for inhibiting leukocyte elastase, cathepsin G, trypsin and/or pancreatic elastase
                                                                                                                                                                                                                                                                         DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 104
                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Xaa
/note= "Xaa is unspecified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Xaa is unspecified in the specification"
                                                                                                                                                                                                                          7,
                                                                                                                                                                                                                                                        EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                         43.7%; Score 143; DB 23; Length 107; 48.2%; Pred. No. 1.1e-07;
                                                                                                                                                                                                                          23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human serine protease inhibitor generic sequence #3.
   destruction such as emphysema, rheumatoid arthritis,
                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    AAU75061 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page - ; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0205372.
90US-0581126.
91US-0807769.
94US-0283477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-2001; 2001US-0880529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0262828
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-121475/16.
                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 107
                                                                                                                                                          107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2001056180-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                     AAU75061;
                                                                                                                                                           Sequence
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                      RESULT 39
                                                                                                                                                                                                                                                                                                                                                     AAU75061
8X3333355XX
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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of
                                                                                                                                                                                                                 inhibitor protein sequence #3 of the invention.

Note, This sequence is not shown in the specification but was created by the indexer from the sequence shown in AAU75057 and the information
               inhibitor, trypsin inhibitor and pancreatic elastase inhibitor activities. A disturbance of the protease/protease inhibitor balance may lead to diseases associated with protease-mediated tissue destruction such as emphysema, rheumatoid arthritis, glomerulonephritis, periodontisis, macular dystrophy, and tumour invasion. The invention also comprises analogues of the serine protease inhibitors in which the amino acid sequence is varied so as to improve
                                                                                                                                         the properties of the protein. These improvements include resistence to oxidative inactivation, improved inhibition of pancreatic elastase, improved inhibition of cathepsin G and trypsin. The present sequence represents the generic human serine protease
protein of the invention has leukocyte elastase inhibitor, cathepsin G
                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EPVKGPVST -- KPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New serine protease inhibitors and DNA sequences for treating a
                                                                                                                                                                                                                                                                                                                                             43.7%; Score 143; DB 23; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                               23; Indels
                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.1e-07
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 40; Column 67-68; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53105 standard; Peptide; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0712354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86US-0890526.
                                                                                                                                                                                                                                                                                                                                                          48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0293042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84US-0678822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85US-0803471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87US-0031846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87US-0082962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-678667/66.
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                             107 AA;
                                                                                                                                                                                                                                                                         given in claim 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6132990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elastase.
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB53105
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contributing chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide cadences essent in the isolation and characterisation of the proteins.
Construction of DNA encoding the protease inhibitors. Peptide sequences CAB53098 - AAC97573 and AAC9582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53098 - AAB53122 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors.
CC The protease inhibitors have cytostatic and anti-inflammatory activity.
The serine protease inhibitor protein is useful for treating a protease mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of protein with the biological activity of HUSI (human seminal plasma inhibitor) type I inhibitors encoded on pRH 34.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic cervical inflammation, inflammation associated with excessive mucus prodn.; post-operative bleeding caused by hyperfibrinolysis, and shock. They are esp. suitable for administration as spray or inhalation. The expression control sequence on the DNA fragment in AAN70928 is bound to the 5' end of HUSI cDNA in an expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUSI-type I inhibitors are useful for treating chronic bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appelhans H, Gassen HG, Machleidt W, Seemuller U;
                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                           Score 143; DB 21; Length 108;
Pred. No. 1.1e-07;
4; Mismatches 23; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  new DNA coding sequences, vectors and transformed organisms, useful eg for treating bronchitis or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein with human seminal plasma inhibitor activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bronchitis therapy; cervix inflammation; hyperfibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP70584 standard; Protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 5; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                               43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86DE-3600571.
                                                                                                                                                                                                                                                                                                                                                                                  48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHEF ) GRUNENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1987-222038/32.
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AA;
                                                                                                                                                                                                                                                                                                                            108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN70930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE3600571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heinzel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70584
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ABB50282 standard; Protein; 132 AA

RESULT 43

(first entry)

11-FEB-2002

ABB50282;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis; inhibitor; human; tryptase; vasoactive intestinal peptide; VTP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM; mast cell; asthma; allergic rhinitis; therapy.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of secretory leukocyte protease inhibitor - as inhibitor of tryptase for treating mast cell-mediated conditions such as asthma and allergic rhinitis
                                                                                                                                                                      14 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 129
                                                                                                                                        26
                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "secretory leukocyte protease inhibitor"
                                                                                                                                 EPVKGPVST - - KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
   Score 143; DB 8; Length 132;
Pred. No. 1.3e-07;
                                                                       23; Indels
                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muller DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                              AAR84056 standard; Protein; 132
   43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US11445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Delaria KA,
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26..132
/note= "s
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9608275-A1
                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAR84056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                       Matches
                                                                                                                                                                                                                                                                                                    RESULT 42
                                                                                                                                                                                                                                                                                                                            AAR84056

AAR84056

AAR84056

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epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; dentification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; adenofibroma problem proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;

gene therapy; vaccine.

WO200175177-A2. Homo sapiens.

11-OCT-2001.

Hough CD;

Sherman-Baust CA, Pizer ES,

Morin PJ,

WPI; 2001-626450/72 N-PSDB; ABA83108

(USSH ) US DEPT HEALTH & HUMAN SERVICES

03-APR-2001; 2001WO-US10947. 03-APR-2000; 2000US-194336P.

Ovarian tumour marker gene; human; overexpression; upregulation; Leukocyte protease inhibitor ovarian tumour marker protein, #54

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assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, cystadenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA831081-ABA83122, ABA83180, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting and identifying ovarian tumor, identifying increased risk for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Page 98; 140pp; English.
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Gaps

2;

23; Indels

43.7%; Score 143; DB 17; 48.2%; Pred. No. 1.3e-07; iive 4; Mismatches 23;

Local Similarity 48.2 nes 27; Conservative

Matches

ò

132 AA;

Sequence Query Match

Length 132;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47402-405 represent secretory leukoprotease inactivator (SLPI) proteins which may be used in may be used in gene therapy. SLPI is a major antiprotease present in the lung. A mutation replacing Met73 of the mature protein with Leu renders the protein oxidation resistant. Therefore it can be used to treat patients with chronic obstructive pulmonary disease (COPD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A non-inflammatory vector composition, comprising nucleic acids and antiinflammatory compound, useful for treating inflammatory disorders, e.g. rheumatoid arthirits, emphysema, cystic fibrosis, adult respiratory distress syndrome and asthma
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent proteins encoded by ovarian tumour marker genes of the invention.
                                                                                                                                                                                      74 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNPCEMDGQCKRDLKCCMGMCGKSCVSP 129
                                                                                                                                                             3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
43.7%; Score 143; DB 22; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.3e-07;
Matches 27; Conservative 4; Mismatches 23; Indels
                                                                                           Length 132;
                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Secretory leukoprotease inactivator; SLPI; gene therapy; antiprotease; lung; oxidation resistant; mutation; chronic obstructive pulmonary disease; COPD.
                                                                                             Score 143; DB 22;
Pred. No. 1.3e-07;
                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal peptide
26..132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Mature SLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                      AAB47403 standard; protein; 132 AA.
                                                                                             43.7%;
48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2000; 2000WO-EP13297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0473018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ennist DL, Mina M;
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                     SLPI native immature form.
                                                                                                                           Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-465212/50.
                                                                                                            Best Local Similarity
                                                                 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200148231-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                     19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001
                                                                                                                                                                                                                                                                                                      AAB47403;
                                                                 Sequence
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lu P,
                                                                                                                                                                                                                                        RESULT 44
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Human, cytostatic, gynecological, elastase, cathepsin G, gene therapy, endometriosis, antileukoprotease, ALP; secretory leukoprotease inhibitor, SLPI, alphal-proteinase inhibitor, alphal-PI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to a method for treating endometriosis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subject, comprising administering to the subject an amount of antileukoprocrases (ALP) effective to inhibit the activity of elastase or cathepsin G, thereby inhibiting ectopic implantation of endometrial fragments. The present sequence is human ALP. ALP is also known as secretory leukoprocease inhibitor (SLPI) and alphal-proteinase inhibitor (alphal-PI). ALP plays an important role in the defence of epithelial surfaces against proteolytic damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating and diagnosing endometriosis or promoting embryo implantation comprises determining or modulating antileukoprotease activity in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
74 DPVDTPNPTRRKPGKCPVTYGOCLMLNPPNPCEMDGOCKRDLKCCMGMCGKSCVSP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.7%; Score 143; DB 22; Length 132;
48.2%; Pred. No. 1.3e-07;
tive 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antileukoprotease; antiinflammatory; antiasthmatic;
                                                                                                AAB66864 standard; Protein; 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Antileukoprotease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU11763 standard; Protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1999; 99US-0142157.
27-JUN-2000; 2000US-0605134.
                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000; 2000WO-IB00990.
                                                                                                                                                               10-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Conservative
                                                                                                                                                                                           Human antileukoprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REPR-) REPROGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-138062/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li Z;
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                                                                                                                                                                                                                                                                                                                       WO200101998-A2.
                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neilson L,
                                                                                                                               AAB66864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU11763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56

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The invention relates to diagnosing an inflammatory lung disorder in
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anti allergic; inflammatory lung disorder; cancer; thyroid tumour;
                              emphysema; asthma; bronchitis; allergy; ovarian carcinoma; renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 19; 36pp; English.
                                                                                                                                                                                                                                                                                                                         25-MAY-2001; 2001WO-US17211.
                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2000; 2000US-207104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rastelli L, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-106211/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS17499
                                                                                                                                                                                           WO200190421-A2
                                                                                                                             Homo sapiens
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mammal, comprising comparing the expression of a nucleic acid encoding and antileukoprotease polypeptide in mammal-derived cell population, and expression of a nucleic acid encoding the antileukoprotease in an inflammation positive or negative reference profile. Also a fisclosed are a method for identifying a compound that inhibits lung inflammation comprising providing a cell expression antileukoprotease, contacting the cell whith a test compound and measuring the expression antileukoprotease in the cell, where a decrease in expression in the presence of the test compound compared to that in the absence of the test compound inhibits lung inflammation.

Also disclosed is assessing prognosis of a mammal with a cancer or a structure of the cell in the compound inhibits lung inflammation. nucleic acid encoding the antileukoprotease in a cancer reference profile, where a substantial similarity between the expression of the nucleic acid sequence in mammal-derived cell population and the cancer reference profile indicates an adverse prognosis of the mammal. The method is used for diagnosing an inflammatory lung disorder such as emphysema, asthma, bronchitis, or allergy in a mammal. The compound is useful for treating or preventing an inflammatory disease in a mammal, preferably human, by inhibiting an inflammatory disease in a mammal, in the method binds to an antileukoprotease nucleic acid, and is a nitleukoprotease antibody, or antileukoprotease antisense nucleic acid, and is a natileukoprotease antisense nucleic acid, with thyroid carcinoma, ovarian carcinoma or renal cell carcinoma. The present sequence is a human antileukoprotease. a thyroid tumour, comprising measuring the expression of a nucleic acid encoding the antileukoprotease in a mammal-derived cell population and comparing expression of the nucleic acid to the expression of a

Example 1; Page 74-76; 134pp; English.

132 AA;

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2; Gaps
                                                                                           3 BPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
ch 43.7%; Score 143; DB 23; Length 132; l Similarity 48.2%; Pred. No. 1.3e-07; 27; Conservative 4; Mismatches 23; Indels ;
  Query Match
Best Local 9
                                               Matches
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AAU99881 standard; Protein; 503 AA. RESULT 47 **AAU99881** g

AAU99881;

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malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour anqiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                     'note= "Amino acids 1-394 of human AAT protein"
                                                                                                                                                                                             /note= "Amino acids 1-107 of SLPI"
                                                                                                                                                                                                              /note= "Linker amino acid"
110..503
                                                  Alzheimer's disease; SLAP1; fusionprotein;
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Pemberton P;
                                                                                                                                                                                                                                                                                                    18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                                                                                                                                                                          18-DEC-2000; 2000US-256699P
                                                                                                                                                                                                                                                                                                                                     20-NOV-2001; 2001US-331966P
           07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                         (ARRI-) ARRIVA PHARM INC.
                               SLAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                               Barr PJ, Gibson HL,
                                                                                                                                                                                                                                                                                                                                                                                                    2002-500631/53
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABK88022
                                                                                                                                                                                                                                                            WO200250287-A2
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                 27-JUN-2002.
                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor
                                                                                                                                                                                  Region
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tunnour metastagis and tunnour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the SLAPI fusion protein of This invention relates to a novel fusion protein comprising a first processe inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting procease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, the invention.

503 AA; Sequence

Gaps .. Length 503; Indels 43.7%; Score 143; DB 23; 48.2%; Pred. No. 4.5e-07; tive 4; Mismatches 23; 27; Conservative Best Local Similarity Query Match Matches

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protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion and a second protease inhibitor or its functionally carive protein. The fusion proteins of the invention may act as an inhibitor of procease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidemal ulceration, chronic trement metastasis and tumour angiogenesis, gastric ulceration, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, millian, chronic trements the millian disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rSLAD1; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; ottitis media; ottitis external; HIV; psoriasis; eczema; humannodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel fusion protein comprising a first
                                                              3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Amino acids 1-107 of human AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Human AAT amino acids 1-394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Linker methionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 90-91; 134pp; English.
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                                                                                                                                                                                                                                                                                                                            AAU99884 standard; Protein; 503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glomerulonephritis; hypertension.
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20-NOV-2001; 2001US-331966P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rSLAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barr PJ, Gibson HL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-500631/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200250287-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to be recombinantly produced in sufficient quantities and
bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the rSLAP1 fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis; acute leukemia.
                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                         445 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNPCBMDGQCKRDLKCCMGMCGKSCVSP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis, muscular dystrophy, and tumour invasion
                                                                                                                                                                                       3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA sequence encoding mammalian serine protease inhibitor
                                                                                                                   Score 143; DB 23; Length 503;
Pred. No. 4.5e-07;
4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 8; 37pp; English.
                                                                                                                                                                                                                                                                                                                AAW94482 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisenberg SP,
                                                                                                                       43.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0279056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0031846.
84US-0678822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0279056
                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease inhibitor.
                                                                                                                                       Best Local Similarity 48.23
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-166640/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bandyopadhyay PK,
                                                                                      503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5871956-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1986;
03-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                  AAW94482;
                                                                                          Sequence
                                                                                                                           Query Match
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                 RESULT 49
                                                                                                                                                                                                                                                                                                     AAW94482
                                                                                                                                                                                                                                                                                                                                  8.8666
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Secretary leukocyte protease inhibitor; antibody; Ab; immunoassay;
                                                                                                              (TEIJ ) TEIJIN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TEIJ ) TEIJIN KK.
                                                                                                                                                                                                                                                             53 AA;
                                                                            29-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP04036191-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1990;
                                          JP03279862-A
                                                                                              29-MAR-1990;
                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            13-JUL-1992
                                                           11-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                          AAR22029;
                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                         RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                                                                                 Elastase-inhibiting peptide of low serine protease-inhibiting activity contains C-terminal portion of human polymorphonuclear leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                          Gaps
                                                                     3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is a fragment of human polymorphonuclear leukocyte elastase inhibiting protein (Asn 55-Ala 107). See AAN90354 for nucleotide sequence. See also AAP90384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                human polymorphonuclear leukocyte elastase inhibiting protein.
                                                                                                                                                                       Human polymorphonuclear leukocyte elastase inhibiting protein.
                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 53;
                                          23; Indels
                                                                                                                                                                                                                                                                                                                        <u>ы</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        Ohtsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 43.1%; Score 141; DB 10; ... Similarity 49.0%; Pred. No. 8.9e-08; 24; Conservative 3; Mismatches 22;
                         Score 142; DB 20;
Pred. No. 1.3e-07;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                        Okada M,
                                                                                                                                                                                                                                                                                                                        Masuda K,
                                                                                                                      53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; fig 2; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR20553 standard; peptide; 53
                         / Match 43.4%;
Local Similarity 48.2%;
nes 27; Conservative

    contains C-terminal portioelastase inhibiting protein.

                                                                                                                     AAP90126 standard; protein;
                                                                                                                                                                                                                                                                     88WO-JP01342
                                                                                                                                                                                                                                                                                      87JP-0330219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                        Kamimura T,
                                                                                                                                                                                                                                                                                                                                        WPI; 1989-220549/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                        Elastase inhibitor;
                                                                                                                                                                                                                                                                                                      (TEIJ ) TEIJIN LTD.
        107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 AA;
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN90354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLPI C-terminal
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                     28-DEC-1988;
                                                                                                                                                                                                                                                                                     28-DEC-1987;
                                                                                                                                                      01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1992
                                                                                                                                                                                                                                                                                                                        Sugiyama T,
                                                                                                                                                                                                                                  WO8906239-A
                                                                                                                                                                                                                                                   13-JUL-1989
                                                                                                                                      AAP90126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR20553;
         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                          Matches
                                                                                                     RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 51
                                                                                                              AAP90126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR2055
XX os
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An anti-human SLPI antibody specific to the C-terminal of human SPLI was prepd. SPLI has neutrophil elastase inhibiting activity. The C-terminal comprises amino acids 55-107 of SPLI. The antibody may be used in an immunoassay for the diagnosis and the treatment of inflammatory diseases, esp. lung diseas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-human secretory leucocyte protease inhibitor antibody recognises peptide with neutrophil elastase inhibiting activity, for diagnosis and treatment of inflammatory diseases e.g. lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PTRRKPGKCPVIYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.1%; Score 141; DB 13; Length
49.0%; Pred. No. 8.9e-08;
tive 3; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulphidation, reproducible, high yield.
neutrophil; elastase; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR22029 standard; peptide; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-0141523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elastase inhibiting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90JP-0141523
                                                                                                                                                                                                                                                            90JP-0081591
                                                                                                                                                                                                                                                                                                                             90JP-0081591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.0°
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-092898/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
The active elastase inhibiting polypeptide was prepd. by sulphonating inactive elastase inhibiting polypeptide obtd. by genetic engineering, and direct disulphidation of the obtd. sulphoderivative without passing through the thiol deriv. stage. The active elastase inhibiting polypeptide has an activity ratio for trypsin inhibiting activity against elastase inhibitory activity of at least 1,000. The active elastase inhibiting polypeptide may be produced in high yield and with good reducibility.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood coagulation inhibitor, inhibits cathepsin G activity and release of serotonin - useful in anti-platelet aggregation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.1%; Score 141; DB 14; Length 53; 49.0%; Pred. No. 8.9e-08;
                                                                                                                                                                               Score 141; DB 13; Length 53;
Pred. No. 8.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serotonin release; secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                         2 PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                           PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cathepsin G activity; inhibitor; platelet aggregation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in anti-platelet aggregation or anti-thrombus drugs.
                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood coagulation inhibitor polypeptide.
                                                                                                                                                                                                                                                                                                                                                       AAR30482 standard; protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4; 5pp; Japanese.
                                                                                                                                                                               43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-0105809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91JP-0105809.
                                                                                                                                                                   Query Match
Best Local Similarity 49.08
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-thrombus drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                               53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP04334325-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     AAR30482;
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50

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RESULT 54 AAW01847

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AAW01843-W01851 are peptides derived from the C-terminal portion of human antileukoprotease. The peptides inhibit the action of tryptase clara. Tryptase clara is responsible for the activation of viruses that have exosporium glycoproteins, such as those that infect the respiratory tract. The peptides are useful for the treatment and prevention of, for example, influenza, parainfluenza, respiratory syncytial virus (RSV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                       Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral; respiratory tract; lung disease; respiratory syncytial virus; RSV; influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antileukoprotease, tryptase clara, carboxyl terminal, virus, viral, respiratory tract, lung disease, respiratory syncytial virus, RSV, influenza, Haemophilus influenzae, mumps, measles, paramyxovirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tryptase clara inhibitor comprises anti:leuko:protease fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treatment and prevention of tryptase clara activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.1%; Score 141; DB 18; Length 53;
49.0%; Pred. No. 8.9e-08;
tive 3; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antileukoprotease derived tryptase clara inhibitor.
                                                                                          Antileukoprotease derived tryptase clara inhibitor
                                                                                                                                                                                                                                                                                                                                                                                        Tashiro M;
AAW01847 standard; peptide; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 22; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW01850 standard; peptide; 53
                                                                                                                                                                                                                                                                                                                                                                                    Kido H,
                                                                                                                                                                                                                                                                                              96WO-JP02071.
                                                                                                                                                                                                                                                                                                                            95JP-0186094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exosporium glycoprotein.
                                                                                                                                                                      exosporium glycoprotein.
                                                                                                                                                                                                                                                                                                                                                         (TANB ) TOKYO TANABE CO.
                                                                                                                                                                                                                                                                                                                                                                                        Imamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-132378/12.
                                                                                                                       Antileukoprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mumps and measles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AA;
                                                                                                                                                                                                                                  WO9703694-A1.
                                                                                                                                                                                                                                                                                              24-JUL-1996;
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                            24-JUL-1995;
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                              AAW01847;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                  Tryptase clara inhibitor comprises anti:leuko:protease fragment -useful for treatment and prevention of tryptase clara activated viral diseases of the respiratory tract, e.g. influenza, RSV, mumps and measles
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PTRRKPGKCPVTYGQCRMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor analogue peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   / Match 43.1%; Score 141; DB 18; Local Similarity 49.0%; Pred. No. 8.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                    Tashiro M;
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                                                                                                                                                                                                                                       Claim 2; Page 24; 40pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB53103 standard; Peptide; 57
                                                                                                                    Kido H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-0293042.
84US-0678822.
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                                                               95JP-0186094
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                                                                                        (TANB ) TOKYO TANABE CO.
                                                                                                                    Imamura Y,
                                                                                                                                             WPI; 1997-132378/12
                                                                                                                                                                                                                                                                                                                                               mumps and measles
                                                                                                                                                                                                                                                                                                                                                                           53 AA;
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                                     24-JUL-1996;
                                                               24-JUL-1995;
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06-DEC-1984;
            06-FEB-1997.
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30-MAR-1987
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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97531 and AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the protease inhibitors. Primars AAC97535 - AAC976373 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences ABE30308 - AAC97632 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease inhibitor protein suseful for treating a protease inhibitor protein suseful for treating a protease activity, the physema arthritis, glomerulonephritis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                              or
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                                       reating a
emphysema
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                                   New serine protease inhibitors and DNA sequences for treating protease-mediated condition or tissue destruction e.g. emphysetumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.1%; Score 141; DB 21; Length 57;
49.0%; Pred. No. 9.5e-08;
tive 3; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins, especially by recombinant methods.
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                                                                                                                       Claim 36; Column 65-66; 47pp; English
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WPI; 2000-678667/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AA;
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                                               AAW01843-W01851 are peptides derived from the C-terminal portion of human antileukoprotease. The peptides inhibit the action of tryptase clara is responsible for the activation of viruses that excessorium glycoproteins, such as those that infect the respiratory tract. The peptides are useful for the treatment and prevention of, for example, influenza, parainfluenza, respiratory syncytial virus (RSV),
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                                                                                                                                                                                                                              43.1%; Score 141; DB 18; Length 58; 49.0%; Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                                  7 PTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 55
                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAW01845 standard; peptide; 58 AA.
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                  Claim 2; Page 25; 40pp; Japanese.
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Les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exosporium glycoprotein.
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                                                                                                                                                        mumps and measles
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                             PEFNPTRRKPGKCPVTYGQCRLLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 55
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45.3%; Pred. No. 1.2e-07;
tive 4; Mismatches 25; Indels
PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
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                                                                                                             AAW01846 standard; peptide; 58 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6132990-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1986
                              05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1987
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB53106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elastase.
                                                                                                                   ſu Ρ,
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB53106
                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                 The sequences given in AAB47402-405 represent secretory leukoprotease inactivator (SLPI) proteins which may be used in may be used in gene therapy. SLPI is a major antiprotease present in the lung. A mutation replacing Met/3 of the mature protein with Leu renders the protein oxidation resistant. Therefore it can be used to treat patients with chronic obstructive pulmonary disease (COPD).
                                                                                                                                                                                                                                              A non-inflammatory vector composition, comprising nucleic acids and antiliflammatory compound, useful for treating inflammatory disorders, e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult respiratory distress syndrome and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                        42.8%; Score 140; DB 22; Length 107;
46.4%; Pred. No. 2.2e-07;
tive 5; Mismatches 23; Indels
Secretory leukoprotease inactivator; SLPI; gene therapy; antiprotease; lung; oxidation resistant; mutation; chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secretory leukoprotease inactivator; SLPI; gene therapy; antiprotease; lung; oxidation resistant; mutation; chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Signal peptide
26..132
/label= oxidation-resistant SLPI
                                                                                                                                                                            (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLPI oxidation-resistant immature form.
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB47405 standard; protein; 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= M73L
                                                                             /label= M73L
                                                                                                                                       27-DEC-2000; 2000WO-EP13297
                                                                                                                                                          99US-0473018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-2001 (first entry)
                                                                                                                                                                                                          Lu P, Ennist DL, Mina M;
                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                             WPI; 2001-465212/50.
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       107 AA;
                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                 WO200148231-A2
                                         Homo sapiens
                                                                                                                                                          28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                   05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB47405;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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The sequences given in AAB47402-405 represent secretory leukoprotease inactivator (SLPI) proteins which may be used in may be used in gene therapy. SLPI is a major antiprotease present in the lung. A mutation replacing Met73 of the mature protein with Leu renders the protein oxidation resistant. Therefore it can be used to treat patients with chronic obstructive pulmonary disease (COPD).
                                                                                                                                                                                                                                                                                                                                                                       A non-inflammatory vector composition, comprising nucleic acids and antinflammatory compound, useful for treating inflammatory disorders, e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 DPVDTPNPTRRKPGKCPVTYGQCLLLNPPNPCEMDGQCKRDLKCCMGMCGKSCVSP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 42.8%; Score 140; DB 22; Length 132;
1 Similarity 46.4%; Pred. No. 2.7e-07;
26; Conservative 5; Mismatches 23; Indels
                                                                                                                            (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory distress syndrome and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 13; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB53106 standard; Peptide; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0293042.
84US-0678822.
85US-0803471.
86US-0890526.
87US-0031846.
87US-0082962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human SLPI peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0712354
27-DEC-2000; 2000WO-EP13297
                                                                99US-0473018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                       Ennist DL, Mina M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN BOULDER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       WPI; 2001-465212/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 AA;
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WPI; 2001-637974/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW00663;
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW00663
   ð
                                                                                                                                                                 This invention relates to new purified and isolated mammalian serine protease inhibitors are capable of and on more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include obligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53122 represent the protease inhibitors Peptide sequences various other peptides used in the isolation of the protease inhibitors protease inhibitors are inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating protease inhibitor, which includes protease mediated tissue destruction, e.g. emphysem, arthritis, glomerulonephritis, puscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant secretory leukocyte protease inhibitor (SLPI) protein.
                                                                           New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema tumor invasion and for recombinant production of inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 139.5; DB 21; Length 101;
48.1%; Pred. No. 2.3e-07;
tive 3; Mismatches 20; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 PVDTPNPRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PVST-----KPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP
 Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson RC;
Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                          Disclosure; Column 15-17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG65996 standard; Protein; 101 AA.
 Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87US-0031846.
90US-0563832.
94US-0279056.
84US-0678222.
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Matches 26; Conservative
                             WPI; 2000-678667/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                              N-PSDB; AAC97530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS6291662-B1
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05-DEC-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents a secretory leukocyte protease inhibitor (SLPI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor, human; tryptase; vasoactive intestinal peptide; VIP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM, mast cell; asthma; allergic rhinitis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR84055, and AAW00653-W00666 represent fragments and muteins of human
secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis;
                                                            New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutein #1 of secretory leukocyte protease inhibitor residues 5-102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of secretory leukocyte protease inhibitor - as inhibitor of tryptase for treating mast cell-mediated conditions such as asthma and allergic rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 139.5; DB 22; Length 101; 48.1%; Pred. No. 2.3e-07; tive 3; Mismatches 20; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PVST-----KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 PVDTPNPRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 99
                                                                                                                                                                                                                                                                               Disclosure; Columns 13-18; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muller DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "L72R"
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N-PSDB; AA167489, AA167491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-179729/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
Les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA;
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length wild type sequence). This sequence represents a Leu-72-Arg mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the substrate over time. By comparing the cleavage of the substrate in the presence and the absence of the test substrance determines as to whether
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98 AA; Sequence

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Gaps
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                                                                                    3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
42.5%; Score 139; DB 17; Length 98; 49.1%; Pred. No. 2.6e-07; tive 4; Mismatches 21; Indels
                                  21; Indels
               Best Local Similarity 49.1
Matches 26; Conservative
 Query Match
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AAW00664 standard; peptide; 98 AA (first entry) 28-OCT-1996 AAW00664; AAW00664 RESULT 

Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis; inhibitor; human; tryptase; vasoactive intestinal peptide; VIP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM; mast cell; asthma; allergic rhinitis; therapy. Mutein #2 of secretory leukocyte protease inhibitor residues 5-102.

Synthetic

Location/Qualifiers /note= "L72K" Misc-difference

WO9608275-A1

21-MAR-1996

95WO-US11445. 11-SEP-1995;

94US-0304051 12-SEP-1994;

(FARB ) BAYER CORP.

Muller DK; Delaria KA, Brownell E,

WPI; 1996-179729/18.

Use of secretory leukocyte protease inhibitor - as inhibitor of tryptase for treating mast cell-mediated conditions such as asthma and allergic rhinitis

Claim 19; ; 65pp; English.

AAR84055, and AAW00653-W00666 represent fragments and muteins of human secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full length wild type sequence). This sequence represents a Leu-72-Lys mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the

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substrate over time. By comparing the cleavage of the substrate in the presence and the absence of the test substance determines as to whether the substance is a tryptase inhibitor. The tryptase substrate used is preferably vasoactive intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or peptide histidine-methionine (PHM). Mast cell, or an active managed conditions in a mammal can be treated by administering an active fragment of SLPI (such as this sequence) or a mutein to the mammal. These conditions include asthma and allergic rhinitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                       42.5%; Score 139; DB 17; Length 98;
49.1%; Pred. No. 2.6e-07;
live 4; Mismatches 21; Indels
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Best Local Similarity 49.1'
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                             98 AA;
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Secretory leukocyte protease inhibitor (SLPI) (see AAR84055 for full secretory leukocyte protease inhibitor (SLPI) (see AAR84056 for full length wild type sequence). This sequence represents a Leu-19-Lys mutein of residues 5-102 of SLIP. SLPI is a potent inhibitor of the proteolytic activity of tryptase. These tryptase inhibitors were identified by incubation with a tryptase containing material and a tryptase substrate. The mixture is then monitored for cleavage of the substrate over time. By comparing the cleavage of the substrate in the presence and the absence of the test substrace determines as to whether the substrace is a tryptase inhibitor. The tryptase substrate used is preferably vasoactive intestinal peptide (VIP), calcitonin gene-related peptide (CGRP) or peptide histidine-methionine (PHM). Mast cell, or tryptase, mediated conditions in a mammal can be treated by administering an active fragment of SLPI (such as this sequence) or a mutein to the mammal. These conditions include asthma and allergic rhinitis.
tryptase, mediated conditions in a mammal can be treated by administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretory leukocyte protease inhibitor; SLPI; N-terminus; proteolysis; inhibitor; human; tryptase; vasoactive intestinal peptide; VIP; CGRP; calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM; mast cell; asthma; allergic rhinitis; therapy.
                 e fragment of SLPI (such as this sequence) or a mutein to the These conditions include asthma and allergic rhinitis.
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                                                                                                                                                                                                                          45 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSC 97
                                                                                                             42.5%; Score 139; DB 17; Length 98, 49.1%; Pred. No. 2.6e-07;
                                                                                                                                                  4; Mismatches
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                                                                                                                                Local Similarity 49.19
nes 26; Conservative
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                                                                           98 AA;
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                                                                                                                                                                                                                                                                                                                                                      inhibitor; human; tryptase; vasoactive incestinal peptide, VIP, CGRP, calcitonin gene-related peptide; peptide histidine-methionine; mammal; PHM, mast cell; asthma; allergic rhinitis; therapy.
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                                   Gaps
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                                                                     3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                      45 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCBMDGQCKRDLKCCMGMCGKSC 97
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 Length 98;
                                                                                                                                                                                                                                                                                                   Residues 5-102 of secretory leukocyte protease inhibitor.
                                   Indels
42.5%; Score 139; DB 17;
49.1%; Pred. No. 2.6e-07;
tive 4; Mismatches 21;
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                                     Conservative
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Best Local Simi
Matches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                  AAW00662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                              RESULT 68
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3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53

ò g

45 DPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSC

97

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Arg
                                                                                                                                                                                                                                                         Lys, Gly, Leu, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a serine protease inhibitor protein comprising a 108 amino acid sequence of formula (I): R1-Gly-Lys-Ser-Phe-
                                                                                                                                                                                                                                                                                              Lys, Gly, Leu,
                                                                                                                                                                                              label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
                                                                                                                                                                                                                                                                                                               Lys, Gly, Arg
                                                                                                                                                                                                                                                                                                                                                                     Tyr, Trp, Lys, Gly, Arg
                                                                                                                                                                                                                                                                                                                                                                                       'label= Met, Val, Ala, Phe, Tyr, Trp, Lys, Gly, Arg
                                                                                         Human, leukocyte elastase inhibitor; parotid secretion; emphysema; serine protease inhibitor; protease/protease inhibitor imbalance; pulmonary disease; polymorphonuclear granulocyte protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New serine protease inhibitor protein used in the treatment
                                                                                                                                                                                                                                                                          Trp,
                                                                                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                                                                        Phe, Tyr, Trp,
                                                                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                                                                                                                              Tyr,
                                                                                                                                                                                                                                                                           Tyr,
                                                                                                                                                                                                                                                                                              Tyr,
                                                                       Human serine protease inhibitor generic sequence.
                                                                                                                                                                                                                                                                                                             Phe,
                                                                                                                                                                                                                                                                           Phe,
                                                                                                                                                                                                                                                                                              Phe,
                                                                                                                                                                                                                                                                                                                                                                      Val, Ala, Phe,
                                                                                                                                                                                                                                                                                                                                   Asp
                                                                                                                                                                                                                                                                                                                                                    Gln
                                                                                                                                                                                                                    Trp
                                                                                                                                                                                                                                                       /label= Met, Val, Ala,
                                                                                                                                                                                                                                                                           Ala,
                                                                                                                                                                                                                                                                                                               Ala,
                                                                                                                                                                                                                                                                                              Ala,
                                                                                                                                                                                                                                                                                                                                                    Glu,
                                                                                                                                                                                                                  /label= Leu, Glu, Gln,
                                                                                                                                                                                                                                     'label= Tyr, Glu, Asp
                                                                                                                                                           Location/Qualifiers
                AAY17425 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                           Val,
                                                                                                                                                                                                                                                                                            Val,
                                                                                                                                                                                                                                                                                                                                  Lys,
                                                                                                                                                                                                                                                                                                                                                    Lys,
                                                                                                                                                                                                                                                                                                              label= Met, Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 15; 12pp; English
                                                                                                                                                                              label= Ser, Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88US-0205372.
84US-0678823.
85US-0803423.
90US-0581126.
91US-0807769.
                                                                                                                                                                                                                                                                         label= Met,
                                                                                                                                                                                                                                                                                            label= Met,
                                                                                                                                                                                                                                                                                                                                 label= Leu,
                                                                                                                                                                                                                                                                                                                                                   label= Leu,
                                                                                                                                                                                                                                                                                                                                                                    label= Met,
                                                                                                                                                                                                                                                                                                                                                                                                          /label= Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0283477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsson K, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-346413/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMGE-) AMGEN INC.
                                                                                                                                                                    Misc-difference
                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1994;
                                                      30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          US5900400-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1999
                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emphysema
                                    AAY17425;
RESULT 69
         AAY17425
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Lys-Ala-Gly-Val-Cys-Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-R2-Tyr-Lys-Lys-Lyc-Bro-Glu-Cys-Glu-Cys-Glu-Sap-R10-Gln-Cys-Pro-Gly-Lys-Arg-Cys-Cys-Pro-Asp-Thr-Arg-Arg-Cys-Cys-Gly-Lys-Arg-Cys-Cys-Pro-Asp-Thr-R2-Gly-Gln-Cys-R8-R3-R9-Asp-Thr-Arg-Arg-Lys-Pro-Gly-Lys-Pro-Pro-Pro-Arg-Arg-Lys-Pro-Gly-Lys-Pys-Pro-Gly-Gln-Cys-R8-R3-R9-Asp-Pro-Pro-Cys-Gly-Lys-Cys-Cys-Lys-R9-R3-R9-R3-R9-R5-Gly-R8-Pro-Gly-Lys-Cys-Cys-Val-Lys-R7 where R1 = serine or proline; R2-R6 = methionine, valine, alanine, phenylalanine, tyrosine, tryptophan, lysine, glycine or arginine; R7 = alanine or proline; R8, S9 = methionine, valine, phenylalanine, tyrosine, tryptophan, lysine, glycine or arginine; R1 = leucine, lysine, glutamine or tryptophan; R1 = leucine, lysine, glutamine or aspartic acid, glutamine or tryptophan; R1 = leucine, lysine, glutamine or aspartic acid, plutamine or aspartic acid, plutamine or aspartic acid, plutamine or aspartic acid, plutamine as compared to parotid secretion-derived serine protease inhibitor in which R10 is tryptophan, R11 is aspartic acid, R12 is leucine, and R13 is tyrosine. (I) is used in the treatment of pulmonary diseases involving protease inhibitor imbalance, preferably emphyseman (I) can be used in the treatment of glutamine argannlocyte protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic sequence capable of directing microbial synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EPVKGPVST -- KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic DNA sequences for directing microbial synthesis
                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the protein encoded by the second exon of AAN60465.
See also AAN60464, AAN60466-69 and AAP60562-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson
                                                                                                                                                                                                                                                                                                                                                                                                           42.2%; Score 138; DB 20; 44.6%; Pred. No. 3.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 19; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP60566 standard; protein; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85WO-US02385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85WO-US02385.
84US-0678822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNE-) SYNERGEN BIOLOG INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85US-0803471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 44.6
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsin-; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1986-169458/26.
                                                                                                                                                                                                                                                                                                                                                                        107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN60465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sandyopadh PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8603519-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP60566;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine
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Sequence Query Match Local

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12 Matches

ઠે g AAR50084;

AAR50084

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AARSB594 is the Arg59-Ala107 section of secretory leukocyte protease inhibitor (SLPI), both it and the sequence described in AARSB595 can used in the treatment of respiratory obstruction. Used orally or parenterally they are particulary useful in the treatment of chronic bronchitis, pulmonary emphysema and asthma.
                                                                                                                                  Secretory leukocyte protease inhibitor; SLPI; asthma; chronic bronchitis; pulmonary emphysema; respiratory obstruction.
                                                                                                Secretory leukocyte protease inhibitor derivative, Arg59-Ala107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secretory leukocyte protease inhibitor; interstitial pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                           Agent to treat respiratory obstruction e.g. in asthma - contg. polypeptide of specified sequence derived from secretory leukocyte protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.6%; Score 136; DB 15; Length 49; 51.1%; Pred. No. 2.7e-07; tive 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory leukocyte protease inhibitor partial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 KPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 46
AAR58594 standard; protein; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75184 standard; peptide; 49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 9; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-0227092.
                                                                                                                                                                                                                                                                                                                          93JP-0012652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1995 (first entry)
                                                                  09-MAY-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-299701/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TEIU ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                            (TEIG ) TEIGIN LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-1993;
                                                                                                                                                                                                                                                                                            28-JAN-1993;
                                                                                                                                                                                                                                                                                                                            28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-1993;
                                                                                                                                                                                                                        JP06228000-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-1995.
                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 73
AAR75184
ID AAR75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secretory Leukoprotease Inhibitor (SLPI) amino acids Arg59-Ala107 inhibits elastase and cathepsin G and does not inhibit trypsin. The cpd. may be used for treating diseases associated with excessive activation of the neutrophil or neutrophil-releasing protease, esp. inflammation, platelet coagulation thrombosis and/or reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide(s) and fusion proteins inhibiting neutrophil elastase and cathepsin G - useful to treat eg inflammation, thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                   ..
                                                                                                                                                                                                                                                                                                                                                            Blastase; cathepsin G; neutrophil; inflammation; thrombosis; inhibition; reperfusion; Secretory Leukoprotease Inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.6%; Score 136; DB 15; Length 49; 51.1%; Pred. No. 2.7e-07; ive 3; Mismatches 19; Indels
                                   Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 46
                                                                                                                         3 KPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                     KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                 41.6%; Score 136; DB 7;
51.1%; Pred. No. 2.7e-07;
                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 24; 31pp; Japanese.
                                                                                                                                                                                                                        AAR50084 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0355553.
92JP-0212398.
92JP-0212399.
                                                                                                                                                                                                                                                                                                                            Elastase-inhibiting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92JP-0340362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder after ischaemia.
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.39
22.34
28.43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-132044/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TEIG ) TEIGIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AA;
   49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reperfusion, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                SLPI; trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP06080697-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1992;
17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-1994.
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                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Gaps

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WPI; 1995-158906/21.

Sequence Query Match

Matches

RESULT 72 AAR58594

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RESULT 75

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 A novel agent for treatment of interstitial pneumonia contains this polypeptide or AR75185 as an active agent. The peptides are partial sequences of secretory leukcyte protease inhibitor (SLPI). In particular, this polypeptide represents Arg59 to Ala107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating respiratory tract obturation caused by neutrophil endotoxins - using drug containing fragment of {\tt SLPT} polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide fragment of Secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.6%; Score 136; DB 16; Length 49; 51.1%; Pred. No. 2.7e-07; tive 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLPI; secretory leukocyte protease inhibitor; Arg58-Ala107; fragment; treat respiratory tract obturation; neutrophil.
                                                                                                                                                                                                                                     'Match 41.6%; Score 136; DB 16; Length 49; Local Similarity 51.1%; Pred. No. 2.7e-07; les 23; Conservative 3; Mismatches 19; Indels
              Effective treating agent for acute or chronic interstitial pneumonia - contg. secretory leukocyte protease inhibitor
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                                                                                                                                                                                                                                                                                                            12 KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                          2 KPGKCPVTYGQCLMLNPPNPCEMDGQCKRDLKCCMGMCGKSCVSP 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 11; 16pp; Japanese.
                                                                                Claim 1; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66284 standard; protein; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93JP-0089933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AA;
                                                                                                                                                                                                     49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1993;
                                                polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                AAR66284
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AAW01843-W01851 are peptides derived from the C-terminal portion of human antileukoprotease. The peptides inhibit the action of tryptase clara. Tryptase clara is responsible for the activation of viruses that have exosporium glycoproteins, such as those that infect the respiratory tract. The peptides are useful for the treatment and prevention of, for example, influenza, parainfluenza, respiratory syncytial virus (RSV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tryptase clara inhibitor comprises anti:leuko:protease fragment -useful for treatment and prevention of tryptase clara activated viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
                                                                                                                                       Antileukoprotease, tryptase clara; carboxyl terminal; virus; viral; respiratory tract; lung disease; respiratory syncytial virus; RSV; influenza; Haemophilus influenzae; measles; paramyxovirus; exosportium glycoprotein.
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                                                                                                           Antileukoprotease derived tryptase clara inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Tashiro M;
                AAW01848 standard; peptide; 49 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    Kido H,
                                                                                                                                                                                                                                                                                                                       96WO-JP02071.
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                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    (TANB ) TOKYO TANABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-132378/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mumps and measles
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                                                                                                                                                                                                                                                                                                                     24-JUL-1996;
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                                                                                                                                                                                                                         Homo sapiens
                                                                             28-OCT-1997
                                                                                                                                                                                                                                                                                        06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and measles
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                                              AAW01848;
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AAW01848
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